```
Db      1 gaatgtgcaacgatcaagtcagggtatctgtggtatccacccacttttgagcatttatcgat 60

Qy     61 tctatatgtcagggaacatttcaagttatctgttctagcaaggaaaatataaaatacttata 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 tctatatgtcagggaacattttcaagttatctgttctagcaaggaaaatataaaatacttata 120

Qy    121 gttaactatgycctatctacagtgcaactaaaaaactayatttttattcctttccacctgtg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gttaactatggcctatctacagtgcaactaaaaactayatttttattcctttccacctgtg 180

Qy    181 ggtttgtattcatttaccacccctctttttcattcccttttctcacccacacactgtgccggg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ggtttgtattcatttaccacccctctttttcattcccttttctcacccacacactgtgccggg 240

Qy    241 cctcaggcatatactattctactgtctgtctctgtaaggattatcattttagcttccaca 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 cctcaggcatatactattctactgtctgtctctgtaaggattatcattttagcttccaca 300

Qy    301 tatgagagaatgcatgcaaagttttttctttccatgtctggcttatttcacttaacataat 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 tatgagagaatgcatgcaaagttttttctttccatgtctggcttatttcacttaacataat 360

Qy    361 gacctccgcttccatccatgttatttatattacccaatagtgttcataaatatatatataca 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gacctccgcttccatccatgttatttatattacccaatagtgttcataaatatatatataca 420

Qy    421 cacatatataccacattgcatttgtccaattattcattgacggaaaactggttaatgttat 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 cacatatataccacattgcatttgtccaattattcattgacggaaaactggttaatgttat 480

Qy    481 atcgttgctattgtggatagtgctgcaataaacacgcaagtggggatataatttgaagaag 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 atcgttgctattgtggatagtgctgcaataaacacgcaagtggggatataatttgaagaag 540

Qy    541 ttttttgttgatgttcctccaaatttaagattgttttgtctatgtttgtgaaaatggc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ttttttgttgatgttcctccaaatttaagattgttttgtctatgtttgtgaaaatggc 600

Qy    601 gttagtattttcatagagattgcattgaatctgtagattgctttgggtaagtatggttat 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gttagtattttcatagagattgcattgaatctgtagattgctttgggtaagtatggttat 660

Qy    661 tttgatggtattaatttttttcattccatgaagatgagatgtctttccattgtttgtgtcc 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 tttgatggtattaatttttttcattccatgaagatgagatgtctttccattgtttgtgtcc 720

Qy    721 tctacattttctttcatcaaagttttgttgtatttttgaagtagatgtatttcacctttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 tctacattttctttcatcaaagttttgttgtatttttgaagtagatgtatttcacctttat 780

Qy    781 agatcaagtgtattccctaaatatttttatttttgtaactattgtagatgaaattjccttc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 agatcaagtgtattccctaaatatttttatttttgtagctattgtagatgaaattgccttc 840

Qy    841 ttgatttctttttcacttaattcattattagtgtatggaaatgttatggatttttatttg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ttgatttctttttcacttaattcattattagtgtatggaaatgttatggatttttatttg 900

Qy    901 ttggtttttaatcaaaaactgtattaaacttagagttttttgtggagtttttaagttttt 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ttggtttttaatcaaaaactgtattaaacttagagttttttgtggagtttttaagttttt 960

Qy    961 ctagatataagatcatgacatctaccaaaaaaaaaaaaaaa 1001
          |||||||||||||||||||||||||||||||||||||||||
Db    961 ctagatataagatcatgacatctaccaaaaaaaaaaaaaaa 1001


RESULT   3
AAC79472
ID   AAC79472 standard; cDNA; 3101 BP.
XX
AC   AAC79472;
XX
DT   07-FEB-2001  (first entry)
XX
DE   cDNA sequence of human breast tumour clone 65338.
XX
KW   human; breast tumour antigen; cytostatic; immunotherapy;
KW   breast cancer; vaccine; ss.
XX
OS   Homo sapiens
XX
PN   WO200061756-A2.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US09088.
XX
PR   09-APR-1999;   99US-0288950.
PR   02-JUL-1999;   99US-0346327.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Reed SG, Xu J, Dillon DC;
XX
DR   WPI; 2000-656558/61.
XX
PT   A novel isolated polypeptide comprising an immunogenic portion of a
PT   breast cancer protein useful in the detection and treatment of breast
PT   cancer.
XX
PS   Claim 4; Page 89-90; 95pp; English.
XX
CC   The present sequence was isolated from a breast tumour cDNA library. It
CC   is provided in a specification relating to compounds for immunotherapy
CC   and diagnosis of breast cancer. Breast tumour antigens and the
CC   polynucleotides that encode them may be used in the production of a
CC   pharmaceutical composition to be used in the treatment of breast cancer.
CC   Proliferated T cells and incubated antigen presenting cells are also
CC   required. The polypeptides and polynucleotides may also be used to
CC   produce a vaccine.
XX
SQ   Sequence 3101 BP; 857 A; 531 C; 491 G; 1222 T; 0 other;


  Query Match           37.3%;  Score 373;  DB 21;  Length 3101;
  Best Local Similarity   99.3%;  Pred. No. 6e-138;
  Matches  813;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    2;

Qy    176 ctatgggtttgtattcatttaccacccctctttttcattcccttttctcacccacacactgtg 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 ctgtgggtttgtattcatttaccacccctctttttcattcccttttctcacccacacactgtg 2343

Qy    236 ccgggcctcaggcatatactattctactgtctgtctctgtaaggattatcattttagctt 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 ccgggcctcaggcatatactattctactgtctgtctctgtaaggattatcattttagctt 2403

Qy    296 ccacatatgagagaatgcatgcaaagttttttctttccatgtctggcttatttcacttaac 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 ccacatatgagagaatgcatgcaaagttttttctttccatgtctggcttatttcacttaac 2463

Qy    356 ataatgacctccgcttccatccatgttatttatattacccaatagtgttcataaatatat 415
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2463 aaaatgacctccgcttccatccatgttatttatattacccaatagtgttcataaatatat 2522

Qy    416 atacacacatatataccacattgcatttgtccaattattcattgacggaaaactggttaat 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2523 atacacacatatataccacattgcatttgtccaattattcattgacggaaaactggttaat 2582

Qy    476 gttatatcgttgctattgtggatagtgctgcaataaacacgcaagtggggatataatttg 535
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   2583 gttatatcgttgctattgtgaatagtgctgcaataaacacgcaagtggggatataatttg 2642

Qy    536 aagagttttttgttgatgttcc-tccaaattttaagattgttttgtctatgtttgtgaa 594
          |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
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Db   2643 aagagtttttttgttgatgttccatacaaatttttaagattgttttgtctatgtttgtgaa 2702

Qy    595 aatggcgttagtatttttcatagagattgcattgaatctgtagattgctttgggtaagtat 654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2703 aatggcgttagtatttttcatagagattgcattgaatctgtagattgctttgggtaagtat 2762

Qy    655 ggttattttgatggtattaatttttttcattccatgaagatgagatgtctttcca-ttgtt 713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| 
Db   2763 ggttattttgatggtattaatttttttcattccatgaagatgagatgtctttccatttgtt 2822

Qy    714 tgtgtcctctacatttttcttttcatcaaagttttgttgtatttttgaagtagatgtatttc 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2823 tgtgtcctctacatttttcttttcatcaaagttttgttgtatttttgaagtagatgtatttc 2882

Qy    774 accttatagatcaagtgtattccctaaatatttttatttttgtagctattgtagatgaaat 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2883 accttatagatcaagtgtattccctaaatatttttatttttgtagctattgtagatgaaat 2942

Qy    834 tgccttcttgatttctttttcacttaattcattattagtgtatggaaatgttatggattt 893
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2943 tgccttctcgatttctttttcacttaattcattattagtgtatggaaatgttatggattt 3002

Qy    894 ttatttgttggttttaatcaaaaactgtattaaacttagagttttttgtggagttttta 953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3003 ttatttgttggttttaatcaaaaactgtattaaacttagagttttttgtggagttttta 3062

Qy    954 agtttttctagatataagatcatgacatctaccaaaaaa 992
          |||||||||||||||||||||||||||||||||||||||
Db   3063 agtttttctagatataagatcatgacatctaccaaaaaa 3101


RESULT   4
AAC27257/c
ID   AAC27257 standard; cDNA; 305 BP.
XX
AC   AAC27257;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 31332.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 31332; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 305 BP; 139 A; 55 C; 34 G; 76 T; 1 other;


  Query Match             3.2%;  Score 32;  DB 21;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    618 gattgcattgaatctgtagattgctttgggta 649
          ||||||||||||||||||||||||||||||||
Db     97 GATTGCATTGAATCTGTAGATTGCTTTGGGTA 66


RESULT   5
AAS10873
ID   AAS10873 standard; cDNA; 41100 BP.
XX
AC   AAS10873;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human genomic DNA containing the NOV6 gene.
XX
KW   Human; NOV6; ds; 78847267; fertility disorder; spermatogenesis;
KW   cardiant; cytostatic; immunomodulatory; antiproliferative;
KW   antidiabetic; cell proliferation; cancer; diabetic retinopathy;
KW   angiogenic disorder; pulmonary disorder; haematopoietic  disorder;
KW   immunological disorder; inflammatory disorder; tumour related disorders;
KW   emphysema; cirrhosis; wound healing; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200149729-A2.
XX
PD   12-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-US00299.
XX
PR   06-JAN-2000; 2000US-0174724.
PR   11-JAN-2000; 2000US-0175434.
PR   11-JAN-2000; 2000US-0175488.
PR   12-JAN-2000; 2000US-0175696.
PR   12-JAN-2000; 2000US-0175743.
PR   13-JAN-2000; 2000US-0175819.
PR   07-AUG-2000; 2000US-0223524.
PR   04-JAN-2001; 2001US-0223524.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Prayaga SK,  Majumder K,  Taillon BE,  Spaderna SK,  Spytek KA;
PI   MacDougall J;
XX
DR   WPI; 2001-418356/44.
XX
PT   Nucleic acids encoding polypeptides, designated NOVX polypeptides,
PT   useful for treating a syndrome associated with a NOVX-associated
PI   disorder, e.g. cell proliferation (e.g. cancer and diabetic
PI   retinopathy), angiogenic or pulmonary disorder -
XX
PS   Disclosure; Page 22-30; 144pp; English.
XX
CC   The invention relates to nucleic acids encoding NOVX (X being an integer
CC   from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
CC   useful in diagnosing, treating or manufacturing a medicament for a
CC   disease or disorder associated with NOVX e.g. cell proliferation (cancer
CC   and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
```

CC disorders (e.g of spermatogenesis), haematopoietic, immunological,
CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
CC healing. NOVX nucleic acids are also useful in gene therapy. They are
CC also used for screening for a modulator of activity or of
CC latency or predisposition to a NOVX-associated disorder. They are also
CC useful for determining the presence of or predisposition to a
CC NOVX-associated disorder. The present sequence contains the gene
CC for NOV6 (7d847267), which has sequence homology to interleukin 6.
XX
SQ Sequence 41100 BP; 12250 A; 8060 C; 8159 G; 12631 T; 0 other;

Query Match 3.0%; Score 30; DB 22; Length 41100;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 338 tggcttatttcacttaacataatgacctcc 367
||||||||||||||||||||||||||||||
Db 39805 tggcttatttcacttaacataatgacctcc 39834

RESULT 6
AAC59199
ID AAC59199 standard; cDNA; 1308 BP.
XX
AC AAC59199;
XX
DT 30-JAN-2001 (first entry)
XX
DE Human secreted protein cDNA sequence #43.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ss.
XX
OS Homo sapiens.
XX
PN WO200055201-A1.
XX
PD 21-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06059.
XX
PR 12-MAR-1999; 99US-0124096.
PR 03-DEC-1999; 99US-0168622.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-628182/60.
DR P-PSDB; AAB27724.
XX
PT Novel human secreted proteins useful for diagnosis, prevention and
PT treatment of disorders including neurological, cell proliferative,
PT cardiovascular, autoimmune/inflammatory disorders and microbial
PT infections
XX
PS Claim 1; Page 362; 427pp; English.
XX
CC The invention relate to the isolation of genes AAC59157-C59205 encoding
CC 49 human secreted proteins AAB27682-B27730. The genes can be used to
CC generate fusion proteins by linking to the gene for the human
CC immunoglobulin G Fc portion for increasing the stability of
CC the fusion protein as compared to the human protein only. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated
CC from a range of human tissues disclosed in the specification. The
CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
SQ Sequence 1308 BP; 322 A; 227 C; 286 G; 472 T; 1 other;

Query Match 2.9%; Score 29; DB 21; Length 1308;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 gattgcattgaatctgtagattgctttgg 646
|||||||||||||||||||||||||||||
Db 740 gattgcattgaatctgtagattgctttgg 768

RESULT 7
AAQ59633/c
ID AAQ59633 standard; cDNA; 319 BP.
XX
AC AAQ59633;
XX
DT 16-MAR-1994 (first entry)
XX
DE Human brain Expressed Sequence Tag EST01493.
XX
KW Gene transcription product; genetic markers; tagging; in vivo;
KW transcription; mapping; locations; chromosomes; chromosomal; ss.
XX
OS Homo sapiens.
XX
PN WO9316178-A.
XX
PD 19-AUG-1993.
XX
PF 12-FEB-1993; 93WO-US01294.
XX
PR 12-FEB-1992; 92US-0837195.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
PI Adams MD, Moreno RF, Venter CJ;
XX
DR WPI; 1993-272882/34.
XX
PT Enriched oligonucleotides and corresp. sequences - used as
PT markers for human genes transcribed in-vivo, facilitate tagging
PT of most human genes
XX
PS Example 4; Page 207; 500pp; English.
XX
CC The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for mapping locations of expressed genes
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prepn. of antisense sequences, probes and constructs.
CC EST01493 has a "poor" coding probability as evaluated using the
CC coding-region prediction program CRM. See also AAQ59041-Q61440.
XX
SQ Sequence 319 BP; 118 A; 42 C; 75 G; 82 T; 2 other;

Query Match 2.7%; Score 27; DB 14; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     341 cttatttcacttaacataatgacctcc 367
           ||||||||||||||||||||||||||||
Db      90 CTTAITTCACTTAACATAATGACCTCC 64


RESULT   8
AAF92122
ID   AAF92122 standard; cDNA; 1177 BP.
XX
AC   AAF92122;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1928 cDNA.
XX
KW   Human; PRO protein; mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   07-DEC-1999;   99US-0169495.
PR   09-DEC-1999;   99US-0170262.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   03-MAR-2000; 2000US-0187202.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   05-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   P-PSDB; AAB87590.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping.
XX
PS   Claim 2; Fig 129; 278pp; English.
XX
CC   The present sequence is the coding sequence for a human PRO polypeptide
CC   (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC   antagonists or anti-PRO antibodies are useful for preparation of a
CC   medicament useful in the treatment of a condition which is responsive to
CC   the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC   protein may also be employed as molecular weight markers for protein
CC   electrophoresis. The PRO coding sequence has applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping.
XX
SQ   Sequence 1177 BP; 272 A; 307 C; 226 G; 372 T; 0 other;


  Query Match             2.7%;  Score 27;  DB 22;  Length 1177;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataatgac 363
           |||||||||||||||||||||||||||
Db    1073 ctggcttatttcacttaacataatgac 1099


RESULT   9
AAD05647
ID   AAD05647 standard; cDNA; 1162 BP.
XX
AC   AAD05647;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Human secreted protein-encoding gene 21 cDNA clone HDPTW65, SEQ ID NO:79.
XX
KW   Human; secreted protein; proliferative disorder; cancer; tumour;
KW   foetal abnormality; developmental abnormality; haematopoietic disorder;
KW   immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW   inflammation; allergy; neurological disorder; Alzheimer's disease;
KW   Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW   skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW   cardiovascular disorder; angiogenic disorder; kidney disorder;
KW   gastrointestinal disorder; pregnancy-related disorder;
KW   endocrine disorder; infection; wound healing; vulnerary;
KW   cell culture; chemotaxis; food additive; gene therapy;
KW   binding partner identification; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             407..553
FT                   /*tag= a
FT                   /product= "Human secreted protein"
FT                   /transl_except= (pos:449..451, aa:Xaa)
FT                   /transl_except= (pos:491..493, aa:Xaa)
FT                   /note= "Xaa equals any of the twenty naturally ocurring
FT                   L-amino acids"
FT   sig_peptide     407..451
FT                   /*tag= b
FT   mat_peptide     452..550
FT                   /*tag= c
FT                   /product= "Human mature secreted protein"
XX
PN   WO200134627-A1.
XX
PD   17-MAY-2001.
XX
PF   08-NOV-2000; 2000WO-US30626.
XX
PR   12-NOV-1999;   99US-0164744.
PR   30-JUN-2000; 2000US-0215140.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Komatsoulis GA, Baker KP, Young PE;
XX
DR   WPI; 2001-316491/33.
DR   P-PSDB; AAE01838.
XX
PT   New nucleic acid molecules encoding human secreted proteins, used in
PT   preventing, treating or ameliorating a disorder, e.g. Alzheimer's di..
PT   Parkinson's diseases and cancers
XX
PS   Claim 1; Page 474; 567pp; English.
XX
CC   AAD05579-AAD05658 represent cDNAs corresponding to 28 human secreted
CC   protein genes and AAE01770-AAE01849 represent the proteins they encode.
CC   AAE01850-AAE01860 represent human secreted protein fragments or variants.
CC   The genes and their secreted proteins are useful for preventing,
CC   treating or ameliorating medical conditions, e.g., by protein or gene
CC   therapy. Pathological conditions can be diagnosed by determining the
CC   amount of the new protein in a sample or by determining the presence of
CC   mutations in the new genes. Specific uses are described for each of the
CC   28 genes, based on the tissues in which they are most highly expressed,
CC   and include developing products for the diagnosis or treatment of
CC   proliferative disorders, cancer, tumours, foetal and developmental
```

```
CC   abnormalities, haematopoietic disorders, diseases of the immune system,
CC   AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC   allergies, neurological disorders (e.g., Alzheimer's disease,
CC   Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC   skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC   cardiovascular disorders, angiogenic disorders, kidney disorders,
CC   gastrointestinal disorders, pregnancy-related disorders, endocrine
CC   disorders, and infections. The proteins can also be used to aid wound
CC   healing and epithelial cell proliferation, to prevent skin aging due to
CC   sunburn, to maintain organs before transplantation, for supporting cell
CC   culture of primary tissues, to regenerate tissues, to identify their
CC   cognate ligands or binding partners, and in chemotaxis, and can be used
CC   as a food additive or preservative to modify storage properties.
CC   Antibodies specific for a protein of the invention can be used in
CC   alleviating symptoms associated with the disorders mentioned above, and
CC   in diagnostic immunoassays e.g. radioimmunoassay or enzyme linked
CC   immunosorbent assay (ELISA). The present sequence represents a human
CC   secreted protein-encoding cDNA of the invention.
XX
SQ   Sequence 1182 BP; 274 A; 170 C; 209 G; 519 T; 10 other;


  Query Match              2.7%;  Score 27;  DB 22;  Length 1182;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     618 gattgcattgaatctgtagattgcttt 644
           |||||||||||||||||||||||||||
Db     535 gattgcattgaatctgtagattgcttt 561


RESULT  10
AAD05599
ID   AAD05599 standard; cDNA; 1917 BP.
XX
AC   AAD05599;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Human secreted protein-encoding gene 21 cDNA clone HDPTW65, SEQ ID NO:31.
XX
KW   Human; secreted protein; proliferative disorder; cancer; tumour;
KW   foetal abnormality; developmental abnormality; haematopoietic disorder;
KW   immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW   inflammation; allergy; neurological disorder; Alzheimer's disease;
KW   Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW   skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW   cardiovascular disorder; angiogenic disorder; kidney disorder;
KW   gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW   endocrine disorder; infection; wound healing; vulnerary;
KW   cell culture; chemotaxis; food additive;
KW   binding partner identification; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             236..382
FT                   /*tag= a
FT                   /product= "Human secreted protein"
FT   sig_peptide     236..280
FT                   /*tag= b
FT   mat_peptide     281..379
FT                   /*tag= c
FT                   /product= "Human mature secreted protein"
XX
PN   WO200134627-A1.
XX
PD   17-MAY-2001.
XX
PF   08-NOV-2000; 2000WO-US30628.
XX
PR   12-NOV-1999;   99US-0164744.
PR   30-JUN-2000; 2000US-0215140.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Komatsoulis GA,  Baker KP,  Young PE;
XX
DR   WPI; 2001-316491/33.
DR   P-PSDB; AAE01790.
XX
PT   New nucleic acid molecules encoding human secreted proteins, used in
PT   preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PI   Parkinson's diseases and cancers -
XX
PS   Claim 1; Page 436-437; 567pp; English.
XX
CC   AAD05579-AAD05658 represent cDNAs corresponding to 28 human secreted
CC   protein genes and AAE01770-AAE01849 represent the proteins they encode.
CC   AAE01850-AAE01860 represent human secreted protein fragments or variants.
CC   The genes and their secreted proteins are useful for preventing,
CC   treating or ameliorating medical conditions, e.g., by protein or gene
CC   therapy. Pathological conditions can be diagnosed by determining the
CC   amount of the new protein in a sample or by determining the presence of
CC   mutations in the new genes. Specific uses are described for each of the
CC   28 genes, based on the tissues in which they are most highly expressed,
CC   and include developing products for the diagnosis or treatment of
CC   proliferative disorders, cancer, tumours, foetal and developmental
CC   abnormalities, haematopoietic disorders, diseases of the immune system,
CC   AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC   allergies, neurological disorders (e.g., Alzheimer's disease,
CC   Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC   skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC   cardiovascular disorders, angiogenic disorders, kidney disorders,
CC   gastrointestinal disorders, pregnancy-related disorders, endocrine
CC   disorders, and infections. The proteins can also be used to aid wound
CC   healing and epithelial cell proliferation, to prevent skin aging due to
CC   sunburn, to maintain organs before transplantation, for supporting cell
CC   culture of primary tissues, to regenerate tissues, to identify their
CC   cognate ligands or binding partners, and in chemotaxis, and can be used
CC   as a food additive or preservative to modify storage properties.
CC   Antibodies specific for a protein of the invention can be used in
CC   alleviating symptoms associated with the disorders mentioned above, and
CC   in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC   immunosorbent assay (ELISA). The present sequence represents a human
CC   secreted protein-encoding cDNA of the invention.
XX
SQ   Sequence 1917 BP; 558 A; 286 C; 349 G; 724 T; 0 other;


  Query Match              2.7%;  Score 27;  DB 22;  Length 1917;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     618 gattgcattgaatctgtagattgcttt 644
           |||||||||||||||||||||||||||
Db     364 gattgcattgaatctgtagattgcttt 390


RESULT  11
AAH73960
ID   AAH73960 standard; cDNA; 2781 BP.
XX
AC   AAH73960;
XX
DT   04-OCT-2001  (first entry)
XX
DE   Human helix-destabilising enzyme C20 coding sequence.
XX
KW   Human; helix-destabilising enzyme C20; cytostatic; virucide;
KW   immunodulatory; antiinflammatory; haemostatic; gene therapy;
KW   malignant tumour; haemopathy; HIV infection; immunological disease;
KW   inflammation; ss.
XX
OS   Homo sapiens.
XX
```

```
PN   WO200155403-A1.
XX
PD   02-AUG-2001.
XX
PF   21-JAN-2001; 2001WO-CN00079.
XX
PR   28-JAN-2000; 2000CN-0111591.
XX
PA   (BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.
XX
PI   Mao Y, Xie Y;
XX
DR   WPI; 2001-483253/52.
DR   P-PSDB; AAG64390.
XX
PT   Human helix-destabilizing enzyme C20 and encoded polynucleotide, used
PT   in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation -
XX
PS   Claim 6; Page 29-30; 35pp; Chinese.
XX
CC   The present sequence is the coding sequence for human helix-destabilising
CC   enzyme C20. The enzyme and its coding sequence are useful in the
CC   diagnosis and treatment of malignant tumour, haemopathy, HIV infection,
CC   immunological diseases and various inflammations.
XX
SQ   Sequence 2781 BP; 712 A; 637 C; 595 G; 837 T; 0 other;


  Query Match              2.7%;  Score 27;  DB 22;  Length 2781;
  Best Local Similarity   100.0%;  Pred. No. 0.098;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     334 tgtctggcttatttcacttaacataat 360
           ||||||||||||||||||||||||||||
Db    1122 tgtctggcttatttcacttaacataat 1148


RESULT  12
AAV42558
ID   AAV42558 standard; DNA; 10409 BP.
XX
AC   AAV42558;
XX
DT   09-NOV-1998  (first entry)
XX
DE   Mouse dectin-2 gene.
XX
KW   Dectin-2; dendritic cell; c-type lectin; mouse; immunity; adjuvant;
KW   allergy; autoimmune disease; gene therapy; vaccine; diagnosis;
KW   drug screening; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   promoter        1..146
FT                   /*tag= a
FT                   /note= "(Claim 136)"
FT   exon            147..171
FT                   /*tag= b
FT                   /number= 1
FT   intron          172..632
FT                   /*tag= c
FT                   /number= 1
FT   exon            633..727
FT                   /*tag= d
FT                   /number= 2
FT   intron          728..2223
FT                   /*tag= e
FT                   /number= 2
FT   exon            2224..2324
FT                   /*tag= f
FT                   /number= 3
FT   intron          2325..5746
FT                   /*tag= g
FT                   /number= 3
FT   exon            5747..5898
FT                   /*tag= h
FT                   /number= 4
XX
PN   WO9828332-A2.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-US23761.
XX
PR   20-DEC-1996;   96US-0772440.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Arilzumi K, Takashima A;
XX
DR   WPI; 1998-377594/32.
DR   P-PSDB; AAW63010.
XX
PI   Nucleic acid encoding dendritic cell specific peptide(s) dectin-1
PI   and -2 - useful, e.g. to regulate immune response, as vaccine
PI   adjuvants, for diagnosis and drug screening
XX
PS   Claim 7; Page 159-165; 200pp; English.
XX
CC   This is the murine dendrin-2 gene that codes for a novel murine
CC   dendritic cell (DC) specific member of the C-type lectin family,
CC   termed DC-associated C-type lectin-2, or dectin-2 (see AAW63010),
CC   that is essential for DC-mediated T cell activation. This novel
CC   gene is expressed selectively by long-term DC lines (XS series)
CC   from murine epidermis. Dectin-2 cDNA (see AAV42549) has also been
CC   isolated. The invention provides: dectin-1 and dectin-2
CC   polypeptides (see also AAW63009-22 and AAW69236-37), useful for
CC   purifying T cells, for detecting autoantibodies and for
CC   up-regulating immunity e.g. as vaccine adjuvants; dectin DNA (see
CC   AAV42548-54 and AAV42558-60); expression vectors; recombinant host
CC   cells; probes and primers useful e.g. for identifying human
CC   dectin-like molecules (see AAV42560); antibodies; compounds that
CC   modulate dectin-mediated activation of T cells; transgenic animals
CC   useful for studying dectin function and for drug screening; and
CC   dectin ligands. Dectin expression can be downregulated by
CC   antisense sequences or ribozymes, or by inactivating the dectin
CC   genes by homologous recombination, e.g. abrogation of dectin
CC   expression is useful for treating allergy and autoimmune
CC   disease. Alternatively gene disruption is done in vitro, the
CC   cells pulsed with an antigen, and returned to the patient to
CC   provide long-term non-responsiveness to the antigen. The dectin-2
CC   promoter region can be used to target gene expression to DC. Since
CC   DC are 'professional' antigen-presenting cells, genetic vaccines
CC   targeted to them should not induce tolerance.
XX
SQ   Sequence 10409 BP; 2816 A; 1968 C; 1976 G; 3541 T; 108 other;


  Query Match              2.7%;  Score 27;  DB 19;  Length 10409;
  Best Local Similarity   100.0%;  Pred. No. 0.084;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     618 gattgcattgaatctgtagattgcttt 644
           |||||||||||||||||||||||||||
Db   10352 gattgcattgaatctgtagattgcttt 10378


RESULT  13
AAX83005
ID   AAX83005 standard; DNA; 29604 BP.
XX
AC   AAX83005;
XX
```

```
DT   31-AUG-1999  (first entry)
XX
DE   Partial mouse WRN genomic sequence #1.
XX
KW   Mouse; WRN; Werner's syndrome; detection; diagnosis; autosomal;
KW   recessive disorder; phenotype; ss.
XX
OS   Mus musculus.
XX
PN   WO9724435-A1.
XX
PD   10-JUL-1997.
XX
PF   30-DEC-1996;   96WO-US20785.
XX
PR   12-APR-1996;   96US-0632175.
PR   29-DEC-1995;   95US-0009409.
PR   29-DEC-1995;   95US-0580539.
PR   30-JAN-1996;   96US-0010835.
PR   30-JAN-1996;   96US-0594242.
XX
PA   (DARW-) DARWIN MOLECULAR CORP.
PA   (OSHI/) OSHIMA J.
XX
PI   Fu Y,  Mulligan J,  Oshima J,  Schellenberg GD,  Yu C;
XX
DR   WPI; 1997-363671/33.
XX
PT   Isolated nucleic acid molecule encoding the WRN gene product -
PT   useful for detection and treatment of Werner's syndrome, and related
PT   diseases
XX
PS   Claim 1; Fig 7; 153pp; English.
XX
CC   This sequence represents a fragment of the genomic sequence containing
CC   the coding region for the mouse WRN gene (AAX83004).  The corresponding
CC   human gene (AAX83001) encodes a protein related to Werner's syndrome.
CC   The products can be used for the detection and treatment of Werner's
CC   syndrome (WS), an autosomal recessive disorder with a complex phenotype,
CC   as well as related diseases.
XX
SQ   Sequence 29604 BP; 7634 A; 5861 C; 5985 G; 10123 T; 1 other;

  Query Match             2.7%;  Score 27;  DB 18;  Length 29604;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     618 gattgcattgaatctgtagattgcttt 644
           |||||||||||||||||||||||||||
Db   22046 gattgcattgaatctgtagattgcttt 22072


RESULT  14
AAZ61522/c
ID   AAZ61522 standard; DNA; 44576 BP.
XX
AC   AAZ61522;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Cosmid CVO14 containing rat vasopressin and oxytocin locus.
XX
KW   Oxytoxin expressed sequence tag; 5'-OT EST; obesity; fertility; male;
KW   transgenic animal; human late onset obesity; late onset visceral obesity;
KW   male infertility; wasting; anorexia; cachexia; malabsorptive state;
KW   catabolic state; inflammatory condition; Crohn's disease; AIDS wasting;
KW   burn; cancer; bone disease; vasopressin; oxytocin; ss.
XX
OS   Rattus sp.
XX
PN   WO200009686-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;   99WO-GB02658.
XX
PR   12-AUG-1998;   98GB-0017566.
PR   06-MAY-1999;   99GB-0010522.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Robinson ICAF,  Stoye JP,  Flavell D,  Wells SE,  Le Tissier P;
XX
DR   WPI; 2000-224331/19.
XX
PT   New anti-obesity polypeptide useful for treating obesity or infertility
PT   in mammals -
XX
PS   Claim 5; Page 129-154; 162pp; English.
XX
CC   The present sequence represents cosmid CVO14, which contains the rat
CC   vasopressin and oxytocin locus. The specification describes 5'OT-EST
CC   (oxytoxin expressed sequence tag) polypeptides. The 5'-OT EST gene is
CC   involved in the control of obesity and fertility in males. 5'-OT EST
CC   nucleic acids are useful for producing transgenic animals. The
CC   transgenic animals created serve as a model for human late onset
CC   obesity and other related disorders and are also used for identifying
CC   the genetic cause of obesity. Compounds which modulate 5'-OT EST
CC   expression or activity are useful in the treatment or modulation of
CC   late onset visceral obesity or male infertility particularly in the
CC   disorders related to these conditions such as wasting, or anorexia,
CC   or cachexia associated with prolonged illness, or malabsorptive states
CC   or catabolic states associated with other diseases such as inflammatory
CC   conditions, Crohn's disease or AIDS wasting, or burns, or cancer, or
CC   bone disease.
XX
SQ   Sequence 44576 BP; 12157 A; 10993 C; 10857 G; 10569 T; 0 other;

  Query Match             2.7%;  Score 27;  DB 21;  Length 44576;
  Best Local Similarity   100.0%;  Pred. No. 0.072;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     618 gattgcattgaatctgtagattgcttt 644
           |||||||||||||||||||||||||||
Db   18092 GATTGCATTGAATCTGTAGATTGCTTT 18066


RESULT  15
AAI16817
ID   AAI16817 standard; DNA; 535 BP.
XX
AC   AAI16817;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #6750 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
```

```
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 25; SEQ ID No 6750; 1417pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging
CC   of diseases of the cervix, notably cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 535 BP; 144 A; 127 C; 70 G; 194 T; 0 other;

  Query Match             2.5%;  Score 25;  DB 22;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 0.72;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataatg 361
           |||||||||||||||||||||||||
Db     290 ctggcttatttcacttaacataatg 314


RESULT  16
AAI40430
ID   AAI40430 standard; DNA; 535 BP.
XX
AC   AAI40430;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Probe #9116 used to measure gene expression in human placenta sample.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00663.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta -
XX
PS   Claim 25; SEQ ID No 9116; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENP).
CC   The present sequence is one such probe. The probes are useful for
CC   producing a microarray for predicting, measuring and displaying gene
CC   expression in samples derived from human placenta. The probes are useful
CC   for antenatal diagnosis of human genetic disorders.
XX
SQ   Sequence 535 BP; 144 A; 127 C; 70 G; 194 T; 0 other;


  Query Match             2.5%;  Score 25;  DB 22;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 0.72;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataatg 361
           |||||||||||||||||||||||||
Db     290 ctggcttatttcacttaacataatg 314


RESULT  17
AAI16533
ID   AAI16533 standard; DNA; 554 BP.
XX
AC   AAI16533;
XX
DT   13-OCT-2001  (first entry)
XX
DE   Probe #6466 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 25; SEQ ID No 6466; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging
CC   of diseases of the cervix, notably cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 554 BP; 147 A; 100 C; 113 G; 194 T; 0 other;
```

```
 Query Match             2.5%;  Score 25;  DB 22;  Length 554;
 Best Local Similarity   100.0%;  Pred. No. 0.72;
 Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataatg 361
           |||||||||||||||||||||||||
Db       9 ctggcttatttcacttaacataatg 33


RESULT  18
AAI39509
ID   AAI39509 standard; DNA; 554 BP.
XX
AC   AAI39509;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Probe #8195 used to measure gene expression in human placenta sample.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00663.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta
XX
PS   Claim 25; SEQ ID No 8195; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENe).
CC   The present sequence is one such probe. The probes are useful for
CC   producing a microarray for predicting, measuring and displaying gene
CC   expression in samples derived from human placenta. The probes are useful
CC   for antenatal diagnosis of human genetic disorders.
XX
SQ   Sequence 554 BP; 147 A; 100 C; 113 G; 194 T; 0 other;


  Query Match             2.5%;  Score 25;  DB 22;  Length 554;
  Best Local Similarity   100.0%;  Pred. No. 0.72;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataatg 361
           |||||||||||||||||||||||||
Db       9 ctggcttatttcacttaacataatg 33


RESULT  19
AAD02701
ID   AAD02701 standard; DNA; 27150 BP.
XX
AC   AAD02701;
XX
DT   02-MAY-2001  (first entry)
XX
DE   Human glycosyl sulfotransferase-6 (GST-6) genomic DNA #1.
XX
KW   Human; glycosyl sulfotransferase-6; GST-6; immunosuppressive;
KW   therapy; selectin binding inhibitor; gene therapy; inflammation;
KW   systemic lupus erythematosus; SLE; rheumatoid arthritis; diabetes;
KW   polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis;
KW   glomerulonephritis; myasthenia gravis; Sjogren's syndrome; adrenalitis;
KW   Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia;
KW   demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis;
KW   myocarditis; adult respiratory distress syndrome; eczema; psoriasis;
KW   asthma; hypersensitivity; rheumatic fever; tissue rejection; ds.
XX
OS   Homo sapiens.
XX
PN   WO200106015-A1.
XX
PD   25-JAN-2001.
XX
PF   19-JUL-2000; 2000WO-US19741.
XX
PR   20-JUL-1999;  99US-0144694.
PR   13-JUL-2000; 2000US-0593628.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Rosen SD,  Lee JK,  Hemmerich S;
XX
DR   WPI; 2001-138471/14.
XX
PI   New glycosyl sulfotransferases (GSI)-4alpha, GST-4beta and GST-6 for
PI   diagnostic and therapeutic agent screening applications
XX
PS   Example 2; Page 116-123; 126pp; English.
XX
CC   The present sequence is human glycosyl sulfotransferase-6 (GST-6)
CC   genomic DNA.
CC   GST is a type 2 membrane protein useful for inhibiting a binding event
CC   between a selectin and a selectin ligand, which comprises contacting the
CC   selectin with a non-sulphated selectin ligand, GST and a small molecular
CC   agent that inhibits the sulphation activity of GST. GST is also useful
CC   in inhibiting a selectin mediated binding event. GST is useful in gene
CC   therapy to treat disorders such as acute or chronic inflammation,
CC   systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis
CC   nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes,
CC   glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's
CC   disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious
CC   anaemia, demyelinating diseases, cirrhosis, ulcerative colitis,
CC   dermatitis, myocarditis, regional enteritis, adult respiratory distress
CC   syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis,
CC   bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection
CC   during transplantation.
XX
SQ   Sequence 27150 BP; 8357 A; 5396 C; 5398 G; 7998 T; 1 other;


  Query Match             2.5%;  Score 25;  DB 22;  Length 27150;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataatg 361
           |||||||||||||||||||||||||
Db   23410 ctggcttatttcacttaacataatg 23434


RESULT  20
AAZ93815
ID   AAZ93815 standard; DNA; 144460 BP.
XX
AC   AAZ93815;
```

```
XX
DT   16-AUG-2000  (first entry)
XX
DE   Olfactory receptor operon.
XX
KW   Olfactory receptor protein; olfactory; smell; receptor; binding;
KW   detection; screening; genotyping; biallelic marker; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2406..2600
FT                   /*tag= a
FT                   /label= ORF1
FT   CDS             9711..10658
FT                   /*tag= b
FT                   /label= ORF2
FT   CDS             24851..25369
FT                   /*tag= c
FT                   /label= ORF3
FT   CDS             45714..46661
FT                   /*tag= d
FT                   /label= ORF4
FT   CDS             80198..81115
FT                   /*tag= e
FT                   /label= ORF 5
FT   CDS             96291..96902
FT                   /*tag= f
FT                   /label= ORF6
FT   CDS             110758..111564
FT                   /*tag= g
FT                   /label= ORF7
FT   CDS             122525..122867
FT                   /*tag= h
FT                   /label= ORF8
FT   CDS             132454..133389
FT                   /*tag= i
FT                   /label= ORF9
FT   CDS             143398..143577
FT                   /*tag= j
FT                   /label= ORF10
FT   misc_feature    complement (113644..114063)
FT                   /*tag= k
FT                   /note= "Ubiquitin 1 pseudogene complement"
FT   misc_feature    complement (127489..127854)
FT                   /*tag= l
FT                   /note= "Ubiquitin 2 pseudogene complement"
FT   allele          7521
FT                   /*tag= m
FT                   /note= "Polymorphic base G or T"
FT   allele          8192
FT                   /*tag= n
FT                   /note= "Polymorphic base G or T"
FT   allele          14483
FT                   /*tag= o
FT                   /note= "Polymorphic base A or T"
FT   allele          19625
FT                   /*tag= p
FT                   /note= "Polymorphic base C or T"
FT   allele          20583
FT                   /*tag= q
FT                   /note= "Polymorphic base A or G"
FT   allele          76947
FT                   /*tag= r
FT                   /note= "Polymorphic base A or C"
FT   allele          91088
FT                   /*tag= s
FT                   /note= "Polymorphic base G or C"
FT   allele          91138
FT                   /*tag= t
FT                   /note= "Polymorphic base A or G"
FT   allele          91187
FT                   /*tag= u
FT                   /note= "Polymorphic base A or G"
FT   allele          133998
FT                   /*tag= v
FT                   /note= "Polymorphic base A or G"
FT   allele          140066
FT                   /*tag= w
FT                   /note= "Polymorphic base C or T"
FT   allele          141176
FT                   /*tag= x
FT                   /note= "Polymorphic base A or G"
FT   allele          144033
FT                   /*tag= y
FT                   /note= "Polymorphic base A or G"
XX
PN   WO200021985-A2.
XX
PD   20-APR-2000.
XX
PF   13-OCT-1999;   99WO-IB01729.
XX
PR   14-OCT-1998;   98US-0104299.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L,  Malekzadeh K;
XX
DR   WPI; 2000-317933/27.
XX
PT   New nucleic acids encoding ten different olfactory receptor proteins
PT   and their biallelic markers, are useful in genetic analysis and in
PT   screening for compounds which bind to the receptor proteins
XX
PS   Claim 1; Page 103-141; 155pp; English.
XX
CC   Ten new olfactory receptor proteins and their biallelic markers have
CC   been described. The sequences encoding these receptor proteins and
CC   which contain the biallelic markers can be used for genotyping. The
CC   olfactory receptor proteins can be used to screen for substances
CC   which bind to them. See GENESEQ records AAZ93816-25 and AAY83386-95.
XX
SQ   Sequence 144460 BP; 46068 A; 27088 C; 26615 G; 44676 T; 13 other;


  Query Match             2.5%;  Score 25;  DB 21;  Length 144460;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataatg 361
           |||||||||||||||||||||||||
Db    1698 ctggcttatttcacttaacataatg 1722


RESULT  21
AAH51601
ID   AAH51601 standard; DNA; 319608 BP.
XX
AC   AAH51601;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human chromosome 13q31-q33 genomic nucleotide sequence.
XX
KW   sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33; haplotype;
KW   biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
XX
OS   Homo sapiens.
XX
PN   WO200058510-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-IB00435.
XX
```

```
PR   30-MAR-1999;   99US-0126903.
PR   30-APR-1999;   99US-0131971.
PR   30-APR-1999;   99US-0132065.
PR   14-JUL-1999;   99US-0143928.
PR   27-JUL-1999;   99US-0145915.
PR   29-JUL-1999;   99US-0146452.
PR   29-JUL-1999;   99US-0146453.
PR   28-OCT-1999;   99US-0162288.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D, Blumenfeld M, Chumakov I, Bougueleret L, Bihain B;
PI   Essioux L;
XX
DR   WPI; 2000-619082/59.
XX
PT   Polynucleotides comprising sequences from sbg1 and g35018 biallelic
PT   markers are used for genotyping and detecting schizophrenia or bipolar
PT   disorder and predisposition to these disorders -
XX
PS   Claim 1; Page 409-493; 737pp; English.
XX
CC   AAH51601 represents a human genomic nucleotide sequence comprising sbg1,
CC   g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the
CC   human chromosome 13q31-q33 locus. The nucleotide sequences contain
CC   biallelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and
CC   AAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein
CC   products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018
CC   cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used
CC   to isolate sbg1 cDNAs, while sbg1 exons from different primates are
CC   represented by sequences AAH51642 - AAH51699. Nucleotide sequences of
CC   amplicons which comprise biallelic markers located on the chromosome
CC   13q31-q33 locus are represented in AAH51700 -AAH51817. Biallelic markers
CC   are represented in the sequences by degenerate/undefined base codes. PCR
CC   primers AAH51818 and AAH51819 are used in the isolation of sequences of
CC   the invention. The biallelic marker containing nucleotide sequences are
CC   used to determine the identity of the nucleotide at a biallelic marker in
CC   a sample DNA sequence. The nucleotide sequences may be labelled and used
CC   for genotyping by determining the identity of a nucleotide at a Region
CC   D-related biallelic marker in a biological sample from single or multiple
CC   subjects. By determining the frequency of a biallelic marker in a
CC   population an association between a genotype and a trait, a haplotype and
CC   a trait and a phenotype and a trait can be detected. The sequences can be
CC   used to determine a predisposition to or early onset of schizophrenia or
CC   bipolar disorder or a beneficial response to or side effects related to
CC   treatment against schizophrenia or bipolar disorder.
XX
SQ   Sequence 319608 BP; 101600 A; 56677 C; 58335 G; 102722 T; 274 other;


  Query Match              2.5%;  Score 25;  DB 21;  Length 319608;
  Best Local Similarity   100.0%;  Pred. No. 0.35;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     334 tgtctggcttatttcacttaacata 358
           |||||||||||||||||||||||||
Db  251041 tgtctggcttatttcacttaacata 251065


RESULT  22
AAS09301
ID   AAS09301 standard; DNA; 319608 BP.
XX
AC   AAS09301;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human schizophrenia associated gene g35030 and biallelic markers A1-A71.
XX
KW   Human; g35030; biallelic marker; A1-A71; chromosome 13q31-q33;
KW   schizophrenia; bipolar disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     7938..7958
FT                   /*tag= a
FT                   /note= "Binds primer 99-27943.rp"
FT   primer_bind     8297..8315
FT                   /*tag= b
FT                   /note= "Binds primer 99-27943-150.mis"
FT   misc_binding    8304..8328
FT                   /*tag= c
FT                   /bound_moiety= Probe_99-27943-150
FT   misc_feature    8316
FT                   /*tag= d
FT                   /note= "Biallelic marker A1"
FT   primer_bind     complement (8317..8335)
FT                   /*tag= e
FT                   /note= "Binds primer 99-27943-150.mis complement"
FT   primer_bind     complement (8446..8465)
FT                   /*tag= f
FT                   /note= "Binds primer 99-27943.pu complement"
FT   primer_bind     21365..21385
FT                   /*tag= g
FT                   /note= "Binds primer 99-27935.rp"
FT   primer_bind     21653..21671
FT                   /*tag= h
FT                   /note= "Binds primer 99-27935-193.mis"
FT   misc_binding    21660..21684
FT                   /*tag= i
FT                   /bound_moiety= Probe_99-27935-193
FT   misc_feature    21672
FT                   /*tag= j
FT                   /note= "Biallelic marker A2"
FT   primer_bind     complement (21673..21691)
FT                   /*tag= k
FT                   /note= "Binds primer 99-27935-193.mis complement"
FT   primer_bind     complement (21845..21864)
FT                   /*tag= l
FT                   /note= "Binds primer 99-27935.pu complement"
FT   primer_bind     65463..65471
FT                   /*tag= m
FT                   /note= "Binds primer 8-128.pu"
FT   primer_bind     65466..65484
FT                   /*tag= n
FT                   /note= "Binds primer 8-128-33.mis"
FT   misc_binding    65473..65497
FT                   /*tag= o
FT                   /bound_moiety= Probe_8-128-33
FT   misc_feature    65485
FT                   /*tag= p
FT                   /note= "Biallelic marker A3"
FT   primer_bind     complement (65486..65504)
FT                   /*tag= q
FT                   /note= "Binds primer 8-128-33.mis complement"
FT   primer_bind     complement (65856..65874)
FT                   /*tag= r
FT                   /note= "Binds primer 8-128.rp complement"
FT   primer_bind     95034..95053
FT                   /*tag= s
FT                   /note= "Binds primer 99-31960.pu"
FT   primer_bind     95377..95395
FT                   /*tag= t
FT                   /note= "Binds primer 99-31960-363.mis"
FT   misc_binding    95384..95408
FT                   /*tag= u
FT                   /bound_moiety= Probe_99-31960-363
FT   misc_feature    95396
FT                   /*tag= v
FT                   /note= "Biallelic marker A4"
FT   primer_bind     complement (95397..95415)
FT                   /*tag= w
FT                   /note= "Binds primer 99-31960-363.mis complement"
FT   primer_bind     complement (95543..95563)
FT                   /*tag= x
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```
FT                   /note= "Binds primer 99-31960.rp complement"
FT   primer_bind     107022..107040
FT                   /*tag= y
FT                   /note= "Binds primer 99-24656.pu"
FT   primer_bind     107262..107280
FT                   /*tag= z
FT                   /note= "Binds primer 99-24656-260.mis"
FT   misc_binding    107269..107293
FT                   /*tag= aa
FT                   /bound_moiety= Probe_99-24656-260
FT   misc_feature    107281
FT                   /*tag= ab
FT                   /note= "Biallelic marker A5"
FT   primer_bind     complement (107282..107300)
FT                   /*tag= ac
FT                   /note= "Binds primer 99-24656-260.mis complement"
FT   primer_bind     complement (107495..107513)
FT                   /*tag= ad
FT                   /note= "Binds primer 99-24656.rp complement"
FT   primer_bind     160279..160298
FT                   /*tag= ae
FT                   /note= "Binds primer 99-24639.rp"
FT   primer_bind     160621..160639
FT                   /*tag= af
FT                   /note= "Binds primer 99-24639-163.mis"
FT   misc_binding    160628..160652
FT                   /*tag= ag
FT                   /bound_moiety= Probe_99-24639-163
FT   misc_feature    160640
FT                   /*tag= ah
FT                   /note= "Biallelic marker A6"
FT   primer_bind     complement (160641..160659)
FT                   /*tag= ai
FT                   /note= "Binds primer 99-24639-163.mis complement"
FT   primer_bind     160770..160787
FT                   /*tag= aj
FT                   /note= "Binds primer 99-24634.pu"
FT   primer_bind     complement (160785..160802)
FT                   /*tag= ak
FT                   /note= "Binds primer 99-24639.pu complement"
FT   primer_bind     160857..160875
FT                   /*tag= al
FT                   /note= "Binds primer 99-24634-108.mis"
FT   misc_binding    160864..160888
FT                   /*tag= am
FT                   /bound_moiety= Probe_99-24634-108
FT   misc_feature    160876
FT                   /*tag= an
FT                   /note= "Biallelic marker A7"
FT   primer_bind     complement (160877..160895)
FT                   /*tag= ao
FT                   /note= "Binds primer 99-24634-108.mis complement"
FT   primer_bind     complement (161240..161257)
FT                   /*tag= ap
FT                   /note= "Binds primer 99-24634.rp complement"
FT   primer_bind     168813..168830
FT                   /*tag= aq
FT                   /note= "Binds primer 99-7652.pu"
FT   primer_bind     168955..168973
FT                   /*tag= ar
FT                   /note= "Binds primer 99-7652-162.mis"
FT   misc_binding    168962..168986
FT                   /*tag= as
FT                   /bound_moiety= Probe_99-7652-162
FT   misc_feature    168974
FT                   /*tag= at
FT                   /note= "Biallelic marker A8"
FT   primer_bind     complement (168975..168993)
FT                   /*tag= au
FT                   /note= "Binds primer 99-7652-162.mis complement"
FT   primer_bind     complement (169331..169351)
FT                   /*tag= av
FT                   /note= "Binds primer 99-7652.rp complement"
FT   primer_bind     170666..170686
FT                   /*tag= aw
FT                   /note= "Binds primer 99-16100.pu"
FT   primer_bind     170791..170809
FT                   /*tag= ax
FT                   /note= "Binds primer 99-16100-147.mis"
FT   misc_binding    170798..170822
FT                   /*tag= ay
FT                   /bound_moiety= Probe_99-16100-147
FT   misc_feature    170810
FT                   /*tag= az
FT                   /note= "Biallelic marker A9"
FT   primer_bind     complement (170811..170829)
FT                   /*tag= ba
FT                   /note= "Binds primer 99-16100-147.mis complement"
FT   primer_bind     complement (171153..171173)
FT                   /*tag= bb
FT                   /note= "Binds primer 99-16100.rp complement"
FT   primer_bind     173065..173085
FT                   /*tag= bc
FT                   /note= "Binds primer 99-5862.rp"
FT   primer_bind     173339..173357
FT                   /*tag= bd
FT                   /note= "Binds primer 99-5862-167.mis"
FT   misc_binding    173346..173370
FT                   /*tag= be
FT                   /bound_moiety= Probe_99-5862-167
FT   misc_feature    173358
FT                   /*tag= bf
FT                   /note= "Biallelic marker A10"
FT   primer_bind     complement (173359..173377)
FT                   /*tag= bg
FT                   /note= "Binds primer 99-5862-167.mis complement"
FT   primer_bind     complement (173495..173514)
FT                   /*tag= bh
FT                   /note= "Binds primer 99-5862.pu complement"
FT   primer_bind     189753..189771
FT                   /*tag= bi
FT                   /note= "Binds primer 99-5919.pu"
FT   primer_bind     189938..189956
FT                   /*tag= bj
FT                   /note= "Binds primer 99-5919-215.mis"
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  Query Match             2.5%;  Score 25;  DB 22;  Length 319608;
  Best Local Similarity   100.0%;  Pred. No. 0.35;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    334 tgtctggcttatttcacttaacata 358
          |||||||||||||||||||||||||
Db 251041 tgtctggcttatttcacttaacata 251065


RESULT  23
AAC28302
ID   AAC28302 standard; cDNA; 305 BP.
XX
AC   AAC28302;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 32377.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
```

```
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures
XX
PS   Claim 1; SEQ ID 32377; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 305 BP; 80 A; 32 C; 68 G; 124 T; 1 other;


  Query Match             2.4%;  Score 24;  DB 21;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     621 tgcattgaatctgtagattgcttt 644
           ||||||||||||||||||||||||
Db     187 tgcattgaatctgtagattgcttt 210


RESULT  24
AAF27996
ID   AAF27996 standard; DNA; 48000 BP.
XX
AC   AAF27996;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human calcium sensitive potassium channel beta3 subunits coding sequence.
XX
KW   Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW   beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW   chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW   irritable bowel syndrome; Alzheimer's disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200105828-A1.
XX
PD   25-JAN-2001.
XX
PF   18-JUL-2000; 2000WO-US19585.
XX
PR   20-JUL-1999;   99US-0144764.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Uebele V,  Swanson R,  Liu Y,  Lagrutta A;
XX
DR   WPI; 2001-159514/16.
XX
PT   Novel human calcium sensitive potassium channel subunits for
PT   identifying inhibitors and agonists of the potassium channel for use in
PT   treating conditions such as asthma, hypertension, memory disorders,
PT   depression
XX
PS   Claim 3; Fig 8; 89pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC   and beta3d subunits. These can be used to identify inhibitors and
CC   activators of the channels, which can be used in the treatment of
CC   conditions including asthma, diabetes, glaucoma, cerebral ischaemia
CC   Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC   incontinence, migraine and irritable bowel syndrome. The coding sequences
CC   are found at human chromosome 3q23-ter. The present sequence is the
CC   beta3 subunits coding sequence.
XX
SQ   Sequence 48000 BP; 13303 A; 9551 C; 10282 G; 14832 T; 32 other;


  Query Match             2.4%;  Score 24;  DB 22;  Length 48000;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     344 atttcacttaacataatgacctcc 367
           ||||||||||||||||||||||||
Db   41657 atttcacttaacataatgacctcc 41680


RESULT  25
AAS04858/c
ID   AAS04858 standard; DNA; 160271 BP.
XX
AC   AAS04858;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human chromosome 18, BAD18ct22-BAD18cag1.
XX
KW   Human; chr18q; fsh30; bipolar affective disorder; BAD;
KW   neuropsychiatric disorder; antibody; schizophrenia; Alzheimer's disease;
KW   Huntingdon's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    28441..144419
FT                   /*tag= a
FT                   /note= "Interval associated with neuropsychiatric
FT                   disorders"
FT   misc_feature    28441..29265
FT                   /*tag= b
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   primer_bind     28384..28405
FT                   /*tag= c
FT                   /label= BADct22_forward
FT   satellite       28547..28572
FT                   /*tag= d
FT                   /rpt_type= TANDEM
FT                   /note= "BADct22 marker"
FT   primer_bind     complement (28547..28572)
FT                   /*tag= e
FT                   /label= BADct2_reverse
FT   misc_feature    29683..39587
FT                   /*tag= f
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    40284..43253
FT                   /*tag= g
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    43518..46075
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FT                   /*tag= h
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    43518..46075
FT                   /*tag= i
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    47264..52284
FT                   /*tag= j
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    52672..56935
FT                   /*tag= k
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    57032..57726
FT                   /*tag= l
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    58065..59057
FT                   /*tag= m
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    59815..60471
FT                   /*tag= n
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    60870..62451
FT                   /*tag= o
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    62543..63268
FT                   /*tag= p
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    63494..66959
FT                   /*tag= q
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    67964..69670
FT                   /*tag= r
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    70643..70749
FT                   /*tag= s
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    71051..72295
FT                   /*tag= t
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    72858..76408
FT                   /*tag= u
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    76797..77123
FT                   /*tag= v
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    77663..78170
FT                   /*tag= w
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    78463..80173
FT                   /*tag= x
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    80466..81519
FT                   /*tag= y
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    81888..85946
FT                   /*tag= z
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FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    86346..87569
FI                   /*tag= aa
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   CDS             87461..87958
FI                   /*tag= ab
FI                   /product= fsh30_gene_product
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    88674..89188
FI                   /*tag= ac
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    89459..89745
FI                   /*tag= ad
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    90436..92299
FI                   /*tag= ae
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    92406..94789
FI                   /*tag= af
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    95556..100121
FI                   /*tag= ag
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    100530..101382
FI                   /*tag= ah
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    101798..103865
FI                   /*tag= ai
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    101798..103865
FI                   /*tag= aj
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    104486..109841
FI                   /*tag= ak
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    109953..110561
FI                   /*tag= al
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    111000..113462
FI                   /*tag= am
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    113774..116253
FI                   /*tag= an
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    116846..117907
FI                   /*tag= ao
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    117999..118623
FI                   /*tag= ap
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    118865..122881
FI                   /*tag= aq
FI                   /label= EST_matching_region
FI                   /note= "This sequence is specifically claimed"
FI   misc_feature    122978..186088
FI                   /*tag= ar
FI                   /label= EST_matching_region
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FT                   /note= "This sequence is specifically claimed. The
FT                   range given for this feature is as stated in the
FT                   specification but is clearly wrong"
FT   misc_feature    129508..130413
FT                   /*tag= as
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    131138..134228
FT                   /*tag= at
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"

  Query Match             2.4%;  Score 24;  DB 22;  Length 160271;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    334 tgtctggcttatttcacttaacat 357
          ||||||||||||||||||||||||
Db 146997 TGTCTGGCTTATTTCACTTAACAT 146974


RESULT  26
AAS04864/c
ID   AAS04864 standard; DNA; 160271 BP.
XX
AC   AAS04864;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human chromosome 18, BAD18ct22-BAD18cag1.
XX
KW   Human; chr18q; fsh27; bipolar affective disorder; BAD;
KW   neuropsychiatric disorder; antibody; schizophrenia; Alzheimer's disease;
KW   Huntingdon's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    28441..144419
FT                   /*tag= a
FT                   /note= "Interval associated with neuropsychiatric
FT                   disorders"
FT   misc_feature    28441..29265
FT                   /*tag= b
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   primer_bind     28384..28405
FT                   /*tag= c
FT                   /label= BADct22_forward
FT   satellite       28547..28572
FT                   /*tag= d
FT                   /rpt_type= TANDEM
FT                   /note= "BADct22 marker"
FT   primer_bind     complement (28547..28572)
FT                   /*tag= e
FT                   /label= BADct2_reverse
FT   misc_feature    29683..39587
FT                   /*tag= f
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    40284..43253
FT                   /*tag= g
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    43518..46075
FT                   /*tag= h
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    43518..46075
FT                   /*tag= i
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    47264..52284
FT                   /*tag= j
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    52672..56935
FT                   /*tag= k
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    57032..57726
FT                   /*tag= l
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    58065..59057
FT                   /*tag= m
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    59815..60471
FT                   /*tag= n
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    60870..62451
FT                   /*tag= o
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    62543..63268
FT                   /*tag= p
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    63494..66959
FT                   /*tag= q
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    67964..69670
FT                   /*tag= r
FT                   /label= EST_matching_area
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    70643..70749
FT                   /*tag= s
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    71051..72295
FT                   /*tag= t
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    72858..76408
FT                   /*tag= u
FT                   /label= EST_matching_region
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FT   misc_feature    76797..77123
FT                   /*tag= v
FT                   /label= EST_matching_area
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    77663..78170
FT                   /*tag= w
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    78463..80173
FT                   /*tag= x
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    80466..81519
FT                   /*tag= y
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    81888..85946
FT                   /*tag= z
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    86346..87569
FT                   /*tag= aa
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    88674..89188
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FT                   /*tag= ab
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    89459..89745
FT                   /*tag= ac
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    90436..92299
FT                   /*tag= ad
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    92406..94789
FT                   /*tag= ae
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    95556..100121
FT                   /*tag= af
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    100530..101382
FT                   /*tag= ag
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    101798..103865
FT                   /*tag= ah
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    101798..103865
FT                   /*tag= ai
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    104486..109841
FT                   /*tag= aj
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    109953..110561
FT                   /*tag= ak
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    111000..113482
FT                   /*tag= al
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    113774..116253
FT                   /*tag= am
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   CDS             115814..119863
FT                   /*tag= an
FT                   /product= fsh27_gene_product
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    116846..117907
FT                   /*tag= ao
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    117999..118623
FT                   /*tag= ap
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    118865..122881
FT                   /*tag= aq
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    122978..186088
FT                   /*tag= ar
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed. The
FT                   range given for this feature is as stated in the
FT                   specification but is clearly wrong"
FT   misc_feature    129508..130413
FT                   /*tag= as
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT   misc_feature    131138..134226
FT                   /*tag= at
FT                   /label= EST_matching_region
FT                   /note= "This sequence is specifically claimed"
FT

  Query Match             2.4%;  Score 24;  DB 22;  Length 160271;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     334 tgtctggcttatttcacttaacat 357
           ||||||||||||||||||||||||
Db  146967 TGTCTGGCTTATTTCACTTAACAT 146974


RESULT  27
AAS06667/c
ID   AAS06667 standard; DNA; 160271 BP.
XX
AC   AAS06667;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human chromosome 18q, 160kb sequence.
XX
KW   Human; 18q; fsh23; neuropsychiatric disorder; schizophrenia;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   brain tumour; diabetes; angina pectoris; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     28384..28405
FT                   /*tag= a
FT                   /note= "PCR primer BAD18ct22 forward"
FT   misc_feature    28441..29265
FT                   /*tag= b
FT                   /note= "This region is specifically claimed"
FT   misc_feature    29683..39587
FT                   /*tag= c
FT                   /note= "This region is specifically claimed"
FT   misc_feature    28441..144419
FT                   /*tag= d
FT                   /note= "Region associated with neuropsychiatric
FT                   disorders"
FT   primer_bind     complement (28547..28572)
FT                   /*tag= e
FT                   /note= "PCR primer BAD18ct22 reverse"
FT   misc_feature    40284..43253
FT                   /*tag= f
FT                   /note= "This region is specifically claimed"
FT   misc_feature    43518..46075
FT                   /*tag= g
FT                   /note= "This region is specifically claimed"
FT   misc_feature    47264..52284
FT                   /*tag= h
FT                   /note= "This region is specifically claimed"
FT   CDS             51458..63491
FT                   /*tag= i
FT                   /product= "Fsh23"
FT                   /note= "Fsh23 gene region"
FT   misc_feature    52672..56935
FT                   /*tag= j
FT                   /note= "This region is specifically claimed"
FT   misc_feature    57032..57726
FT                   /*tag= k
FT                   /note= "This region is specifically claimed"
FT   misc_feature    58065..59057
FT                   /*tag= l
FT                   /note= "This region is specifically claimed"
FT   misc_feature    59815..60471
FT                   /*tag= m
FT                   /note= "This region is specifically claimed"
FT   misc_feature    60870..62451
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FT                   /*tag= n
FT                   /note= "This region is specifically claimed"
FT   misc_feature    62543..63268
FT                   /*tag= o
FT                   /note= "This region is specifically claimed"
FT   misc_feature    63494..66969
FT                   /*tag= p
FT                   /note= "This region is specifically claimed"
FT   misc_feature    67964..69670
FT                   /*tag= q
FT                   /note= "This region is specifically claimed"
FT   misc_feature    70643..70749
FT                   /*tag= r
FT                   /note= "This region is specifically claimed"
FT   misc_feature    71051..72295
FT                   /*tag= s
FT                   /note= "This region is specifically claimed"
FT   misc_feature    72858..76408
FT                   /*tag= t
FT                   /note= "This region is specifically claimed"
FT   misc_feature    76797..77123
FT                   /*tag= u
FT                   /note= "This region is specifically claimed"
FT   misc_feature    77663..78170
FT                   /*tag= v
FT                   /note= "This region is specifically claimed"
FT   misc_feature    78463..80173
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FT                   /note= "This region is specifically claimed"
FT   misc_feature    80466..81519
FT                   /*tag= x
FT                   /note= "This region is specifically claimed"
FT   misc_feature    81888..85946
FT                   /*tag= y
FT                   /note= "This region is specifically claimed"
FT   misc_feature    86346..87569
FT                   /*tag= z
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FT                   /*tag= aa
FT                   /note= "This region is specifically claimed"
FT   misc_feature    89459..89745
FT                   /*tag= ab
FT                   /note= "This region is specifically claimed"
FT   misc_feature    90436..92299
FT                   /*tag= ac
FT                   /note= "This region is specifically claimed"
FT   misc_feature    92406..94789
FT                   /*tag= ad
FT                   /note= "This region is specifically claimed"
FT   misc_feature    95556..100121
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FT                   /note= "This region is specifically claimed"
FT   misc_feature    100530..101382
FT                   /*tag= af
FT                   /note= "This region is specifically claimed"
FT   misc_feature    101798..103865
FT                   /*tag= ag
FT                   /note= "This region is specifically claimed"
FT   misc_feature    104486..109841
FT                   /*tag= ah
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FT   misc_feature    109953..110561
FT                   /*tag= ai
FT                   /note= "This region is specifically claimed"
FT   misc_feature    111000..113482
FT                   /*tag= aj
FT                   /note= "This region is specifically claimed"
FT   misc_feature    113774..116253
FT                   /*tag= ak
FT                   /note= "This region is specifically claimed"
FT   misc_feature    116846..117907
FT                   /*tag= al
FT                   /note= "This region is specifically claimed"
FT   misc_feature    117959..118623
FT                   /*tag= am
FT                   /note= "This region is specifically claimed"
FT   misc_feature    118865..122881
FT                   /*tag= an
FT                   /note= "This region is specifically claimed"
FT   misc_feature    122978..1860e8
FT                   /*tag= ao
FT                   /note= "This region is specifically claimed.
FT                   This is an erroneous range given that the
FT                   sequence is only 160kb in size"
FT   misc_feature    129506..130413
FT                   /*tag= ap
FT                   /note= "This region is specifically claimed"
FT   misc_feature    131138..134228
FT                   /*tag= aq
FT                   /note= "This region is specifically claimed"
FT   misc_feature    134517..135473
FT                   /*tag= ar
FT                   /note= "This region is specifically claimed"
FT   misc_feature    135815..139983
FT                   /*tag= as
FT                   /note= "This region is specifically claimed"
FT   misc_feature    140583..144419
FT                   /*tag= at
FT                   /note= "This region is specifically claimed"
FT   primer_bind     144302..144325
FT                   /*tag= au
FT                   /note= "PCR primer BAD18cagl forward"
FT   primer_bind     complement (144477..144501)
FT                   /*tag= av
FT                   /note= "PCR primer BAD18cagl reverse"
XX
PN   WO200134772-A2.
XX
PD   17-MAY-2001.
XX
PF   08-NOV-2000; 2000WO-US30819.
XX
PR   08-NOV-1999;   99US-0164042.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chen H, Freimer NB;
XX
DR   WPI; 2001-343601/36.
XX
PT   Novel mammalian fsh23 polynucleotide for diagnostic evaluation, genetic
PT   testing and prognosis of fsh23-related disorders such as
PT   neuropsychiatric disorders including schizophrenia, bipolar affective
PT   disorder
XX
PS   Claim 1; Fig 1B; 196pp; English.
XX
CC   The sequence represents 160kb of human chromosome 18q containing
CC   fsh23 gene, located in a region associated with neuropsychiatric
CC   disorders. The fsh23 gene and polypeptide, its fragment, analog or
CC   mimetic is useful for treating a fsh23-related disorder or fsh23-mediated
CC   process such as neuropsychiatric disorders e.g., schizophrenia,
CC   attention deficit disorder, schizoaffective disorder, bipolar affective
CC   disorder and unipolar disorder. A cell harbouring the gene is engineered
CC   ex vivo to express an unimpaired fsh23 protein. The gene and protein are
CC   also useful for treating neurodegenerative disorders such as Alzheimer's
CC   disease, senile dementia, Huntington's disease, amyotrophic lateral
CC   sclerosis, Parkinson's disease, and Gilles de la Tourette's syndrome, and
CC   hypertension and sleep disorders, mania, obsessive-compulsive disorder,
CC   and anxiety. The gene and protein are also useful for the diagnostic
CC   evaluation, genetic testing and/or prognosis of a fsh23-related disorder,

  Query Match             2.4%;  Score 24;  DB 22;  Length 160271;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
```

```
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     334 tgtctggcttatttcacttaacat 357
           |||||||||||||||||||||||||
Db 146997 TGTCTGGCTTATTTCACTTAACAT 146974


RESULT  28
AAH40997/c
ID   AAH40997 standard; DNA; 160271 BP.
XX
AC   AAH40997;
XX
DT   21-AUG-2001  (first entry)
XX
DE   160kb fragment of the long arm of human chromosome 18q.
XX
KW   Chromosome 18q; fsh25; human; neuropsychiatric disorder; schizophrenia;
KW   attention deficit disorder; schizoaffective disorder; BAD; mania;
KW   bipolar affective disorder; unipolar disorder; depression; ds; BP;
KW   bipolar mood disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (28384..28405)
FT                   /*tag= a
FT                   /note= "BADct22 specific primer"
FT   misc_feature    28440..28483
FT                   /*tag= b
FT                   /note= "BADct22 marker sequence"
FT   primer_bind     28547..28572
FT                   /*tag= c
FT                   /note= "BADct22 specific primer"
FT   CDS             complement (116254..116523)
FT                   /*tag= d
FT                   /product= "fsh25 protein"
FT   primer_bind     complement (144302..144325)
FT                   /*tag= e
FT                   /note= "BAD18cag1 specific primer"
FT   misc_feature    144388..144420
FT                   /*tag= f
FT                   /note= "BAD18cag1 marker sequence"
FT   primer_bind     144477..144501
FT                   /*tag= g
FT                   /note= "BAD18cag1 specific primer"
XX
PN   WO200133965-A1.
XX
PD   17-MAY-2001.
XX
PF   07-NOV-2000; 2000WO-US30636.
XX
PR   08-NOV-1999;   99US-0164038.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chen H,  Freimer NB;
XX
DR   WPI; 2001-308772/32.
XX
PT   Nucleic acids encoding mammalian fsh25 polypeptides associated with
PT   neuropsychiatric disorders, useful for treating e.g. bipolar affective
PT   disorders -
XX
PS   Claim 1; Fig 1B; 153pp; English.
XX
CC   This invention relates to the present sequence which represents a 160kb
CC   fragment of the long arm of human chromosome 18q. The sequence includes
CC   the 18q interval associated with neuropsychiatric disorders (nucleotides
CC   28441-144419). Included in this region is the fsh25 gene, which is
CC   involved in neuropsychiatric disorders. Included in the invention are
CC   fragments of the DNA sequence, and antibodies which bind to its protein
CC   products. Fsh25 DNA and protein sequences, a vector containing the DNA
CC   sequence, and an antibody directed against the protein product may be
CC   used in the prevention, diagnosis and treatment of diseases associated
CC   with inappropriate fsh25 expression. Disorders that may be prevented,
CC   diagnosed and/or treated using the DNA, protein, vector and antibody
CC   include neuropsychiatric disorders, such as schizophrenia, attention
CC   deficit disorder, a schizoaffective disorder, a bipolar affective
CC   disorder or a unipolar disorder.
XX
SQ   Sequence 160271 BP; 45619 A; 32965 C; 34927 G; 46702 T; 58 other;


  Query Match             2.4%;  Score 24;  DB 22;  Length 160271;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     334 tgtctggcttatttcacttaacat 357
           |||||||||||||||||||||||||
Db 146997 TGTCTGGCTTATTTCACTTAACAT 146974


RESULT  29
AAH23764/c
ID   AAH23764 standard; DNA; 160271 BP.
XX
AC   AAH23764;
XX
DT   13-AUG-2001  (first entry)
XX
DE   Human chromosome 18q interval containing the fsh26 gene.
XX
KW   Human; chromosome 18q; fsh26; nootropic; neuroprotective; BAD18ct22;
KW   neuroleptic; hypotensive; gene therapy; BAD18cag1; hypertension;
KW   neuropsychiatric disorder; bipolar affective disorder; schizophrenia;
KW   bipolar mood disorder; manic-depressive illness; Alzheimer's disease;
KW   neurodegenerative disorder; senile dementia; Huntington's disease;
KW   amyotrophic lateral sclerosis; Parkinson's disease; sleep disorder;
KW   Gilles de la Tourette's syndrome; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    28441..29265
FT                   /*tag= a
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    29683..39587
FT                   /*tag= b
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    40284..43253
FT                   /*tag= c
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    43518..46075,
FT                   /*tag= d
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    47264..52284,
FT                   /*tag= e
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    52672..56935,
FT                   /*tag= f
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    57032..57726,
FT                   /*tag= g
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    58065..59057,
FT                   /*tag= h
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    59815..60471,
FT                   /*tag= i
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    60870..62451,
FT                   /*tag= j
FT                   /note= "This sequence is specifically claimed in Claim 1"
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FT   misc_feature    62543..63268,
FT                   /*tag= k
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    63494..66959,
FT                   /*tag= l
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    67964..69670,
FT                   /*tag= m
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    70643..70749,
FT                   /*tag= n
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    71051..72295,
FT                   /*tag= o
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    72858..76408,
FT                   /*tag= p
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    76797..77123,
FT                   /*tag= q
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    77663..78170,
FT                   /*tag= r
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    78463..80173,
FT                   /*tag= s
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    80466..81519,
FT                   /*tag= t
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    81888..85946,
FT                   /*tag= u
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    86346..87569,
FT                   /*tag= v
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    88674..89188,
FT                   /*tag= w
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    89459..89745,
FT                   /*tag= x
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    90436..92299,
FT                   /*tag= y
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    92406..94789,
FT                   /*tag= z
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    95556..100121,
FT                   /*tag= aa
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    100530..101382,
FT                   /*tag= ab
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    101798..103865,
FT                   /*tag= ac
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    104486..109841,
FT                   /*tag= ad
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    109953..110561,
FT                   /*tag= ae
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    111000..113482,
FT                   /*tag= af
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    113774..116253,
FT                   /*tag= ag
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    116846..117907,
FT                   /*tag= ah
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    117999..118623
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FT                   /*tag= ai
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    118665..122881,
FT                   /*tag= aj
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    122978..126088,
FT                   /*tag= ak
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    129508..130413,
FT                   /*tag= al
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    131136..134228,
FT                   /*tag= am
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    134517..135473,
FT                   /*tag= an
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    135815..139583
FT                   /*tag= ao
FT                   /note= "This sequence is specifically claimed in Claim 1"
FT   misc_feature    140683..144419
FT                   /*tag= ap
FT                   /note= "This sequence is specifically claimed in Claim 1"
XX
PN   WO200134641-A1.
XX
PD   17-MAY-2001.
XX
PF   08-NOV-2000; 2000WO-US30824.
XX
PR   08-NOV-1999;   99US-0164037.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chen H, Freimer NB;
XX
DR   WPI; 2001-356946/35.
XX
PT   Novel mammalian fsh26 polynucleotide for diagnostic evaluation, genetic
PT   testing and prognosis of fsh26-related disorders e.g., neuropsychiatric
PT   disorders including schizophrenia and bipolar affective disorder
XX
PS   Claim 1; Fig 1B; 174pp; English.
XX
CC   The present sequence is a 116 kb fragment located between markers
CC   BAD18ct22 and BAD18cag1 from human chromosome 18q. This sequence includes
CC   the 18q interval associated with neuropsychiatric disorders, located from
CC   positions 28441-144419. This sequence also contains a novel gene: fsh26
CC   gene. The fsh26 gene is associated with bipolar affective disorder (BAD;
CC   also known as bipolar mood disorder: BP; or manic-depressive illness) in
CC   humans. The present sequence or its fragment, analog or mimetic is useful
CC   for treating a fsh26-related disorder or fsh26-mediated process in a
CC   mammal, such as neuropsychiatric disorders such as schizophrenia,
CC   attention deficit disorder, schizoaffective disorder, bipolar affective
CC   disorder and unipolar disorder. Also, neurodegenerative disorders such as
CC   Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Parkinson's disease, as well as Gilles de la
CC   Tourette's syndrome, autonomic function disorders such as hypertension
CC   and sleep disorders can be treated.
XX
SQ   Sequence 160271 BP; 45618 A; 32964 C; 34928 G; 46703 T; 58 other;


  Query Match             2.4%;  Score 24;  DB 22;  Length 160271;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     334 tgtctggcttatttcacttaacat 357
           ||||||||||||||||||||||||
Db  146997 TGTCTGGCTTATTTCACTTAACAT 146974
```

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RESULT 30
AAF85116/c
ID   AAF85116 standard; DNA; 160271 BP.
XX
AC   AAF85116;
XX
DT   09-JUL-2001 (first entry)
XX
DE   Nucleotide sequence of 160 kb of chromosome 18q.
XX
KW   BAD18cag1 marker; fsh28 gene; bipolar affective disorder; BAD;
KW   chromosome 18; chromosome 18q; neuropsychiatric disorder; schizophrenia;
KW   attention deficient disorder; schizoaffective disorder;
KW   unipolar disorder; BAD18ct22 marker; ss.
XX
OS   Homo sapiens.
XX
PN   WO200133964-A1.
XX
PD   17-MAY-2001.
XX
PF   07-NOV-2000; 2000WO-US30610.
XX
PR   08-NOV-1999;   99US-0164040.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chen H, Freimer NB;
XX
DR   WPI; 2001-300582/31.
XX
PT   New isolated mammalian nucleic acid for diagnosing, monitoring and
PT   treating neuropsychiatric disorders, such as bipolar affector disorder,
PT   schizophrenia, or attention deficient disorder -
XX
PS   Claim 1; Fig 1B; 155pp; English.
XX
CC   The present sequence represents a 160 kb fragment of the long arm of
CC   chromosome 18. This region is associated with neuropsychiatric disorders,
CC   and contains the fsh28 gene and markers BAD18ct22 and BAD18cag1. The
CC   fsh28 gene is a gene involved in bipolar affective disorder (BAD). The
CC   fsh28 polynucleotides and polypeptides are used to detect, modulate, or
CC   treat chromosome 18q related disorders or fsh-28 related disorders,
CC   such as neuropsychiatric disorders, especially schizophrenia, attention
CC   deficient disorder, a schizoaffective disorder, a bipolar affective
CC   disorder, or a unipolar disorder. They can be use to identify an
CC   individual having or at risk of developing one of the disorders. The
CC   fsh28 gene and derived polynucleotides can be used to identify a
CC   compound capable of modulating fsh28 activity.
XX
SQ   Sequence 160271 BP; 45619 A; 32964 C; 34928 G; 46702 T; 58 other;

  Query Match              2.4%;  Score 24;  DB 22;  Length 160271;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     334 tgtctggcttatttcacttaacat 357
           ||||||||||||||||||||||||
Db 146997 TGTCTGGCTTATTTCACTTAACAT 146974


RESULT 31
AAF93676
ID   AAF93676 standard; cDNA; 553 BP.
XX
AC   AAF93676;
XX
DT   21-MAY-2001 (first entry)
XX
DE   cDNA isolated from foetal brain tissue encoding SRT protein SEQ ID 497.
XX
KW   Human; SRT; gene therapy; gene mapping; tissue typing; ss.
XX
OS   Homo sapiens.
XX
PN   WO200107611-A2.
XX
PD   01-FEB-2001.
XX
PF   21-JUL-2000; 2000WO-US20006.
XX
PR   26-JUL-1999;   99US-0145701.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Goddard A, Wood WI;
XX
DR   WPI; 2001-112729/12.
XX
PT   New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT   for production of recombinant SRT polypeptides, gene mapping,
PT   diagnosing genetic disorders and for gene therapy -
XX
PS   Claim 2; Fig 497; 663pp; English.
XX
CC   Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC   human SRT proteins. The cDNA sequences are isolated from various
CC   different human tissue cDNA libraries. The invention relates to a method
CC   for detecting cDNA encoding an SRT protein, a vector containing cDNA
CC   encoding SRT, a host cell transformed with the vector, an isolated SRT
CC   polypeptide, and an antibody which binds to SRT. The polynucleotide
CC   sequence can be used in gene therapy and is useful in the recombinant
CC   production of SRT polypeptides, as a hybridisation probe to screen
CC   libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC   map the gene encoding the SRT polypeptides and analysing genetic
CC   disorders, tissue typing and disease tissue detection. The SRT
CC   polynucleotide sequences can be used in polymerase chain reaction,
CC   screening for new therapeutic molecules and generation of antisense RNA
CC   and DNA.
XX
SQ   Sequence 553 BP; 156 A; 108 C; 91 G; 198 T; 0 other;

  Query Match              2.3%;  Score 23;  DB 22;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataa 359
           |||||||||||||||||||||||
Db     198 ctggcttatttcacttaacataa 220


RESULT 32
AAC57691/c
ID   AAC57691 standard; DNA; 1001 BP.
XX
AC   AAC57691;
XX
DT   25-JAN-2001 (first entry)
XX
DE   Arachidonic acid metabolism related genomic biallelic marker #525.
XX
KW   Human; biallelic marker; arachidonic acid metabolism; genotyping;
KW   detection; hybridisation; phenotype; haplotype; SNP; polymorphic base;
KW   single nucleotide polymorphism; hybridisation assay; sequencing assay;
KW   specific amplification assay; identification; ERBM; 12-LO-RBM;
KW   eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
XX
OS   Homo sapiens.
XX
PN   WO200047771-A2.
XX
PD   17-AUG-2000.
XX
```

```
PF   11-FEB-2000; 2000WO-IB00184.
XX
PR   12-FEB-1999;   99US-0119917.
PR   23-MAR-1999;   99US-0275267.
PR   07-MAY-1999;   99US-0133200.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M, Bougueleret L, Chumakov I;
XX
DR   WPI; 2000-571881/53.
XX
PT   Novel biallelic markers useful for detecting conditions and genotypes
PT   associated with arachidonic acid metabolism -
XX
PS   Claim 13; Page 673; 802pp; English.
XX
CC   The present invention describes polynucleotides including biallelic
CC   markers derived from genes involved in arachidonic acid metabolism and
CC   from genomic regions flanking those genes. Methods from the present
CC   invention may be used to select individuals for clinical trials and
CC   predict responses to treatment with drugs. The polynucleotides may be
CC   used in hybridisation assays, sequencing assays and specific
CC   amplification assays for identifying an eicosanoid-related biallelic
CC   marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
CC   segment of nucleotides containing an ERBM. The polynucleotides are
CC   useful in diagnostic kits. The markers may be used to detect conditions
CC   and genotypes associated with arachidonic acid metabolism. AAC57367 to
CC   AAC58018 and AAB24019 and AAB24020 represent sequences used in the
CC   exemplification of the present invention.
CC   N.B. Polymorphic bases (single nucleotide polymorphisms also known as
CC   SNPs) in the polynucleotide sequences from the present invention have
CC   been given as their corresponding degenerate bases e.g. a polymorphic
CC   base of C or T has been given as Y.
XX
SQ   Sequence 1001 BP; 305 A; 182 C; 279 G; 234 T; 1 other;

  Query Match             2.3%;  Score 23;  DB 21;  Length 1001;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ctggcttatttcacttaacataa 359
           |||||||||||||||||||||||
Db     995 CTGGCTTATTTCACTTAACATAA 973


RESULT  33
AAD04475
ID   AAD04475 standard; cDNA; 5353 BP.
XX
AC   AAD04475;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Human 27875 ADAM-TS cDNA, alternative version.
XX
KW   Human; ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory;
KW   angiogenesis; bronchial asthma; Goodpasture's syndrome; metastasis;
KW   heart failure; cardiac hypertrophy; chronic ischaemic heart disease;
KW   sickle cell disease nephropathy; urinary tract obstruction; haemostatic;
KW   skeletal muscle disorder; myocardial infarction; blood vessel disorder;
KW   hypertension; atherosclerosis; vasculitis; renal artery stenosis; mumps;
KW   gonorrhea; tuberculosis; syphilis; spermatocytic seminoma; osteoporosis;
KW   rhabdomyosarcoma; glomerulonephritis; bone disorder; Paget's disease;
KW   rickets; osteomalacia; Hodgkin's disease; gene therapy; antibacterial;
KW   cardiant; tumour; thymoma; vasotropic; cytostatic; virucide; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             36..5096
FT                   /*tag= a
FT                   /product= "Human 27875 ADAM-TS protein"
FT                   /transl_except= (pos:1a21..1823, aa:Xaa)
FT                   /note= "Xaa is an unknown amino acid"
FT   sig_peptide     36..125
FT                   /*tag= b
FT   mat_peptide     126..5093
FT                   /*tag= c
FT                   /product= "Human mature 27875 ADAM-TS protein"
XX
PN   WO200131034-A1.
XX
PD   03-MAY-2001.
XX
PF   25-OCT-2000; 2000WO-US29360.
XX
PR   25-OCT-1999;   99US-0426282.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, White D;
XX
DR   WPI; 2001-300513/31.
DR   P-PSDB; AAE00913.
XX
PT   Novel isolated polypeptide, 27875, a human ADAM-TS (a disintegrin and
PT   metalloproteinase) useful for diagnosis and treatment of disorders of
PT   bone, lung, heart, skeletal muscle such as osteoporosis, emphysema,
PT   angina -
XX
PS   Claim 7; Page 115-123; 133pp; English.
XX
CC   The present sequence is an alternative version of a cDNA encoding
CC   27875 protein, a human ADAM-TS (a disintegrin and metalloproteinase).
CC   Metalloproteinase is a proteolytic enzyme involved in protein
CC   maturation, protein degradation, tumour growth, metastasis and
CC   angiogenesis. Nucleotides encoding 27875, 27875 protein and its
CC   antibodies are useful for preventing, diagnosing and treating
CC   27875 metalloproteinase-related disorders. These disorders
CC   include, disorders involving the lung such as congenital anomalies,
CC   bronchial asthma, Goodpasture's syndrome, pulmonary alveolar proteinosis,
CC   disorders involving heart such as heart failure, cardiac hypertrophy,
CC   angina pectoris, myocardial infarction, chronic ischaemic heart disease,
CC   disorders involving the skeletal muscle include tumours such as
CC   rhabdomyosarcoma, disorders involving blood vessel such as hypertension,
CC   atherosclerosis, vasculitis associated with other disorders, disorders
CC   involving the testis and epididymis such as nonspecific epididymitis and
CC   orchitis, gonorrhea, mumps, tuberculosis and syphilis, spermatocytic
CC   seminoma, disorders involving the kidney such as membranoproliferative
CC   glomerulonephritis, necrotising glomerulonephritis, renal artery
CC   stenosis, chronic glomerulonephritis, sickle cell disease nephropathy,
CC   urinary tract obstruction, disorders of the bone such as achondroplasia,
CC   osteoporosis, Paget's disease, rickets, osteomalacia, osteonecrosis,
CC   tuberculous osteomyelitism, osteoma, osteosarcoma, metastatic tumours,
CC   and disorders involving thymus such as thymic cysts, thymic hypoplasia,
CC   thymomas, and Hodgkin's disease. 27875 sequence is used in gene therapy.
CC   Note: This sequence SEQ.ID.NO.2 is stated as being similar to the
CC   sequence shown in Fig 1 (See AAD04494). However these sequences differ
CC   at several locations.
XX
SQ   Sequence 5353 BP; 960 A; 1833 C; 1648 G; 911 T; 1 other;

  Query Match             2.3%;  Score 23;  DB 22;  Length 5353;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     979 catctaccaaaaaaaaaaaaaa 1001
           |||||||||||||||||||||||
Db    5296 catctaccaaaaaaaaaaaaaa 5318


RESULT  34
AAD04494
```

```
ID   AAD04494 standard; cDNA; 5353 BP
XX
AC   AAD04494;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Human 27875 ADAM-TS (a disintegrin and metalloproteinase) cDNA.
XX
KW   Human; ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory;
KW   angiogenesis; bronchial asthma; Goodpasture's syndrome; metastasis;
KW   heart failure; cardiac hypertrophy; chronic ischaemic heart disease;
KW   sickle cell disease nephropathy; urinary tract obstruction; haemostatic;
KW   skeletal muscle disorder; myocardial infarction; blood vessel disorder;
KW   hypertension; atherosclerosis; vasculitis; renal artery stenosis; mumps;
KW   gonorrhea; tuberculosis; syphilis; spermatocytic seminoma; osteoporosis;
KW   rhabdomyosarcoma; glomerulonephritis; bone disorder; Paget's disease;
KW   rickets; osteomalacia; Hodgkin's disease; gene therapy; antibacterial;
KW   cardiant; tumour; thymoma; vasotropic; cytostatic; virucide; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             36..5096
FT                   /*tag= a
FT                   /product= "Human 27875 ADAM-TS protein"
FT   sig_peptide     36..125
FT                   /*tag= b
FT   mat_peptide     126..5093
FT                   /*tag= c
FT                   /product= "Human mature 27875 ADAM-TS protein"
XX
PN   WO200131034-A1.
XX
PD   03-MAY-2001.
XX
PF   25-OCT-2000; 2000WO-US29380.
XX
PR   25-OCT-1999;   99US-0426282.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  White D;
XX
DR   WPI; 2001-300513/31.
DR   P-PSDB; AAE00934.
XX
PT   Novel isolated polypeptide, 27875 a human ADAM-TS (a disintegrin and
PT   metalloproteinase) useful for diagnosis and treatment of disorders of
PT   bone, lung, heart, skeletal muscle such as osteoporosis, emphysema,
PT   angina -
XX
PS   Claim 7; Fig 1; 133pp; English.
XX
CC   The present sequence is a cDNA encoding 27875 protein, a human ADAM-TS
CC   (a disintegrin and metalloproteinase). Metalloproteinase is a
CC   proteolytic enzyme involved in protein maturation, protein degradation,
CC   tumour growth, metastasis and angiogenesis. Nucleotides encoding 27875,
CC   27875 protein and its antibodies are useful for preventing, diagnosing
CC   and treating 27875 metalloproteinase-related disorders. These disorders
CC   include, disorders involving the lung such as congenital anomalies,
CC   bronchial asthma, Goodpasture's syndrome, pulmonary alveolar proteinosis,
CC   disorders involving heart such as heart failure, cardiac hypertrophy,
CC   angina pectoris, myocardial infarction, chronic ischaemic heart disease
CC   disorders involving the skeletal muscle include tumours such as
CC   rhabdomyosarcoma, disorders involving blood vessel such as hypertension,
CC   atherosclerosis, vasculitis associated with other disorders, disorders
CC   involving the testis and epididymis such as nonspecific epididymitis and
CC   orchitis, gonorrhea, mumps, tuberculosis and syphilis, spermatocytic
CC   seminoma, disorders involving the kidney such as membranoproliferative
CC   glomerulonephritis, necrotising glomerulonephritis, renal artery
CC   stenosis, chronic glomerulonephritis, sickle cell disease nephropathy
CC   urinary tract obstruction, disorders of the bone such as achondroplasia,
CC   osteoporosis, Paget's disease, rickets, osteomalacia, osteonecrosis,
CC   tuberculous osteomyelitism, osteoma, osteosarcoma, metastatic tumours
CC   and disorders involving thymus such as thymic cysts, thymic hypoplasia,
CC   thymomas, and Hodgkin's disease. 27875 sequence is used in gene therapy.
CC   Note: This sequence SEQ.ID.NO.2 is stated as being similar to the
CC   sequence shown in Page 115-123 (See AAD04475). However these sequences
CC   differ at several locations.
XX
SQ   Sequence 5353 BP; 960 A; 1833 C; 1649 G; 911 T; 0 other;


  Query Match           2.3%;  Score 23;  DB 22;  Length 5353;
  Best Local Similarity  100.0%;  Pred. No. 3.4;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     979 catctaccaaaaaaaaaaaaaa 1001
           |||||||||||||||||||||||
Db    5296 catctaccaaaaaaaaaaaaaa 5318


RESULT  35
AAC89559/c
ID   AAC89559 standard; DNA; 80331 BP.
XX
AC   AAC89559;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Human histone deacetylase HDAC-C coding sequence.
XX
KW   Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW   HDAC-D; cell cycle; tumourigenesis; cancer; inhibitor; antisense;
KW   gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200071703-A2.
XX
PD   30-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-IB01252.
XX
PR   03-MAY-1999;   99US-0132287.
XX
PA   (METH-) METHYLGENE INC.
XX
PI   Macleod AR,  Li Z,  Besterman JM;
XX
DR   WPI; 2001-016407/02.
DR   P-PSDB; AAB49959.
XX
PT   Antisense oligonucleotide that inhibits expression of a histone
PT   deacetylase, useful for treating and/or alleviating the symptoms of
PT   neoplasia, or for inhibiting neoplastic cell growth in an animal -
XX
PS   Disclosure; Page 66-89; 125pp; English.
XX
CC   The present invention provides inhibitors of histone deacetylase enzymes
CC   such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC   inhibitors may be antisense strands or they may be compounds identified
CC   by contacting the enzyme with the compound and measuring the resulting
CC   enzyme activity. These inhibitors are useful for treating cancers and for
CC   identifying which histone deacetylase is involved in a neoplasia.
XX
SQ   Sequence 80331 BP; 26046 A; 14486 C; 13823 G; 25976 T; 0 other;


  Query Match           2.3%;  Score 23;  DB 22;  Length 80331;
  Best Local Similarity  100.0%;  Pred. No. 2.5;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     628 aatctgtagattgctttgggtaa 650
           |||||||||||||||||||||||
Db   44113 AATCTGTAGATTGCTTTGGGTAA 44091
```

```
RESULT 36
AAC15149
ID   AAC15149 standard; cDNA; 247 BP.
XX
AC   AAC15149;
XX
DT   06-OCT-2000 (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 19224.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 19224; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 247 BP; 55 A; 39 C; 51 G; 97 T; 5 other;

  Query Match              2.2%;  Score 22;  DB 21;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     618 gattgcattgaatctgtagatt 639
           |||||||||||||||||||||||
Db      35 gattgcattgaatctgtagatt 56


RESULT 37
AAC26972
ID   AAC26972 standard; cDNA; 329 BP.
XX
AC   AAC26972;
XX
DT   06-OCT-2000 (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 31047.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 31047; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 329 BP; 80 A; 50 C; 66 G; 132 T; 1 other;

  Query Match              2.2%;  Score 22;  DB 21;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     626 tgaatctgtagattgctttggg 647
           |||||||||||||||||||||||
Db     144 tgaatctgtagattgctttggg 165


RESULT 38
AAZ42729
ID   AAZ42729 standard; cDNA; 329 BP.
XX
AC   AAZ42729;
XX
DT   01-FEB-2000 (first entry)
XX
DE   Human 5' EST isolated from a cDNA library SEQ ID NO:488.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW   gene therapy; chromosome mapping; upstream regulatory sequence;
KW   forensic; location; development; protein synthesis; stability;
KW   regulation; identification; ss.
XX
OS   Homo sapiens.
XX
PN   WO9953051-A2.
XX
PD   21-OCT-1999.
```

```
XX
PF   09-APR-1999;   99WO-IB00712.
XX
PR   09-APR-1998;   98US-0057719.
PR   28-APR-1998;   98US-0069047.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-038446/03.
DR   P-PSDB; AAY65115.
XX
PT   Novel secreted protein 5' expressed sequence tag sequences used in
PT   diagnostic, forensic, gene therapy, and chromosome mapping procedures
XX
PS   Claim 1; Page 427; 837pp; English.
XX
CC   AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
CC   sequences, corresponding to human secreted proteins. AAY64651 to
CC   AAY65438 represent the EST-related proteins corresponding to AAZ42265 to
CC   AAZ43052. The 5' ESTs can be used for producing secreted human gene
CC   products. They can be used to identify and isolate 5' untranslated
CC   regions (UTRs) and upstream regulatory regions which control the
CC   location, development stage, rate, and quantity of protein synthesis, as
CC   well as stability of mRNA. The ESTs are also useful as probes for
CC   chromosome mapping, and to obtain full length cDNA clones. The ESTs can
CC   also be used in forensic procedures to identify individuals, or in
CC   diagnostic procedures to identify individuals having genetic diseases
CC   resulting from abnormal gene expression. The products may also be used in
CC   gene therapy protocols. The nucleic acids encoding signal peptides can be
CC   used for directing extracellular secretion of a polypeptide or the
CC   insertion of a polypeptide into a membrane, or importing a polypeptide
CC   into a cell. The proteins encoded by the EST sequences may be useful in
CC   treating a variety of human conditions. Secreted proteins have
CC   therapeutic value, and the identification of new secreted proteins is
CC   valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent
CC   sequences used in the exemplification of the present invention.
XX
SQ   Sequence 329 BP; 80 A; 50 C; 66 G; 132 T; 1 other;


  Query Match             2.2%;  Score 22;  DB 21;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     626 tgaatctgtagattgctttggg 647
           ||||||||||||||||||||||
Db     144 tgaatctgtagattgctttggg 165


RESULT  39
AAC36471
ID   AAC36471 standard; DNA; 731 BP.
XX
AC   AAC36471;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 13931.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
PR   14-MAY-1999;   99US-0134221.
PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
PR   20-MAY-1999;   99US-0135124.
PR   21-MAY-1999;   99US-0135353.
PR   24-MAY-1999;   99US-0135629.
PR   25-MAY-1999;   99US-0136021.
PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
PR   10-JUN-1999;   99US-0138540.
PR   10-JUN-1999;   99US-0138847.
PR   14-JUN-1999;   99US-0139119.
PR   16-JUN-1999;   99US-0139452.
PR   16-JUN-1999;   99US-0139453.
PR   17-JUN-1999;   99US-0139492.
PR   18-JUN-1999;   99US-0139454.
PR   18-JUN-1999;   99US-0139455.
PR   18-JUN-1999;   99US-0139456.
PR   18-JUN-1999;   99US-0139457.
PR   18-JUN-1999;   99US-0139458.
PR   18-JUN-1999;   99US-0139459.
PR   18-JUN-1999;   99US-0139460.
PR   18-JUN-1999;   99US-0139461.
PR   18-JUN-1999;   99US-0139462.
PR   18-JUN-1999;   99US-0139463.
PR   18-JUN-1999;   99US-0139750.
PR   18-JUN-1999;   99US-0139763.
PR   21-JUN-1999;   99US-0139817.
PR   22-JUN-1999;   99US-0139899.
PR   23-JUN-1999;   99US-0140353.
PR   23-JUN-1999;   99US-0140354.
PR   24-JUN-1999;   99US-0140695.
PR   28-JUN-1999;   99US-0140823.
PR   29-JUN-1999;   99US-0140991.
PR   30-JUN-1999;   99US-0141287.
PR   01-JUL-1999;   99US-0141842.
PR   01-JUL-1999;   99US-0142154.
PR   02-JUL-1999;   99US-0142055.
PR   06-JUL-1999;   99US-0142390.
PR   08-JUL-1999;   99US-0142803.
PR   09-JUL-1999;   99US-0142920.
PR   12-JUL-1999;   99US-0142977.
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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147036.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.

PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.2%; Score 22; DB 21; Length 731;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 410 atatatatacacacatatatac 431
||||||||||||||||||||||
Db 393 atatatatacacacatatatac 414

RESULT 40
AAZ22862
ID AAZ22862 standard; cDNA; 1005 BP.
XX
AC AAZ22862;
XX
DT 20-DEC-1999 (first entry)
XX
DE Wheat indole-3-glycerol phosphate synthase partial cDNA.
XX
KW Tryptophan; biosynthesis; transgenic plant; herbicide;
KW indole-3-glycerol phosphate synthase; ds.
XX
OS Triticum aestivum.
XX
FH Key Location/Qualifiers
FT CDS 1..810
FT /*tag= a
FT /partial
FT /product= "Wheat indole-3-glycerol phosphate synthase"
FT /note= "No initiation codon given in specification"
XX
PN WO9949013-A2.
XX
PD 30-SEP-1999.
XX
PF 22-MAR-1999; 99WO-US06582.
XX
PR 26-MAR-1998; 98US-0079386.

```
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon RE, Falco SC, Gutteridge S, Hitz WD, Maxwell CA;
PI   Rafalski JA, Tao Y, Vollmer SJ;
XX
DR   WPI; 1999-580437/49.
DR   P-PSDB; AAY42527.
XX
PT   New isolated nucleic acids encoding plant enzymes involved in
PT   tryptophan biosynthesis, used to generate transgenic plants, and
PT   enzymes used as herbicide targets -
XX
PS   Claim 7; Page 55-56; 65pp; English.
XX
CC   This sequence represents a wheat indole-3-glycerol phosphate synthase
CC   partial cDNA. Indole-3-glycerol phosphate synthase is an enzyme
CC   involved in the biosynthesis of tryptophan. Plants are able to synthesise
CC   all twenty amino acids, unlike vertebrate animals, which require
CC   certain amino acids (essential amino acids) in their diet as they
CC   cannot manufacture them de novo. Tryptophan is one such essential amino
CC   acid. In plants, the biosynthesis of tryptophan from chorismic acid
CC   requires five enzymatic steps catalysed by anthranilate synthase,
CC   anthranilate phosphoribosyltransferase, phosphoribosylanthranilate
CC   isomerase, indole-3-glycerol phosphate synthase and tryptophan synthase.
CC   The tryptophan pathway leads to the biosynthesis of many secondary
CC   metabolites, including the hormone indole-3-acetic acid, antimicrobial
CC   phytoalexins, alkaloids and glucosinolates. Nucleotides that encode
CC   tryptophan biosynthetic enzymes may be used to generate transgenic
CC   plants in which the expression of tryptophan biosynthetic enzymes is
CC   altered, including plants having an increased tryptophan content or
CC   those which cannot synthesise tryptophan (loss of function mutants).
CC   Recombinant tryptophan biosynthetic enzymes can be used to screen for
CC   specific inhibitors which may be potentially useful as herbicides. As
CC   these enzymes are involved in a biosynthesis pathway that does not exist
CC   in higher animals, they represent an ideal target for herbicides.
XX
SQ   Sequence 1005 BP; 282 A; 189 C; 270 G; 264 T; 0 other;


  Query Match             2.2%;  Score 22;  DB 20;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     980 atctaccaaaaaaaaaaaaaa 1001
           ||||||||||||||||||||||
Db     974 atctaccaaaaaaaaaaaaaa 995


RESULT  41
AAC32953
ID   AAC32953 standard; DNA; 1148 BP.
XX
AC   AAC32953;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 1253.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123546.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
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PR   14-MAY-1999;   99US-0134221.
PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
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PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
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PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
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PR   02-JUL-1999;   99US-0142055.
PR   06-JUL-1999;   99US-0142390.
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PR 15-JUL-1999; 99US-0144005.
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PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
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PR 15-SEP-1999; 99US-0154018.
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PR 20-SEP-1999; 99US-0154779.
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PR 24-SEP-1999; 99US-0155659.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.2%; Score 22; DB 21; Length 1148;
Best Local Similarity 100.0%; Pred. No. 10;
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Qy 410 atatatatacacacatatatac 431
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Db 781 atatatatacacacatatatac 802

RESULT 42
AAH17506/c
ID AAH17506 standard; cDNA; 1796 BP.
XX
AC AAH17506;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:16978.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX

```
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs .
XX
PS   Claim 8; SEQ ID 16978; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 1796 BP; 657 A; 319 C; 372 G; 448 T; 0 other;


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Qy     342 ttatttcacttaacataatgac 363
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RESULT  43
AAQ55138
ID   AAQ55138 standard; DNA; 8654 BP.
XX
AC   AAQ55138;
XX
DT   21-SEP-1995  (first entry)
XX
DE   Staphylococcus epidermidis probe SE-22.
XX
KW   Probe; S.aureus; S.epidermis; E.faecalis; P.aeruginosa; E.coli;
KW   K.pneumoniae; E.cloacae; clinical sample; ds.
XX
OS   Staphylococcus epidermidis.
XX
PN   WO9401583-A.
XX
PD   20-JAN-1994.
XX
PF   07-JUL-1993;   93WO-JP00936.
XX
PR   07-JUL-1992;   92JP-0179719.
XX
PA   (FUSO ) FUSO PHARM IND LTD.
PA   (OHNO/) OHNO T.
XX
PI   Eda S,  Matsuhisa A,  Ohno T,  Uehara H;
XX
DR   WPI; 1994-035086/04.
XX
PI   Probe for identifying bacteria causing infectious disease -
PI   consists of a DNA fragment obtained by HindIII cleavage of the
PI   pathogenic bacterial genomic DNA
XX
PS   Claim 4; Page 30-35; 100pp; Japanese.
XX
CC   The nucleotide sequence of an 8654 bp probe obtained by digestion of
CC   Staphylococcus epidermidis genomic DNA with the restriction enzyme
CC   HindIII.  The probes (AAQ55133-48 and AAQ55752-58) represent other
CC   probes derived, by HindIII digestion of the genomes of S.aureus,
CC   S.epidermis, Enterococcus faecalis, Pseudomonas aeruginosa, E.coli,
CC   Klebsiella pneumoniae or Enterobacter cloacae.  The probes can be used to
CC   detect their respective microorganisms in clinical samples.
XX
SQ   Sequence 8654 BP; 2968 A; 1137 C; 1362 G; 3186 T; 1 other;


  Query Match             2.2%;  Score 22;  DB 15;  Length 8654;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     805 tttatttttgtagctattgtag 826
           ||||||||||||||||||||||
Db    7872 tttatttttgtagctattgtag 7893


RESULT  44
AAI62937
ID   AAI62937 standard; DNA; 11617 BP.
XX
AC   AAI62937;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human genomic DNA SEQ ID NO 265.
XX
KW   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW   immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW   antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW   antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW   antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW   antiparasitic; cardiant;  immune disorder; cardiovascular disorder;
KW   neurological disease; infection; nephrotropic; gene therapy; vaccine.
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200155449-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01346.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUL-2000; 2000US-0216880.
PR   14-JUL-2000; 2000US-0218290.
PR   14-AUG-2000; 2000US-0225447.
PR   01-SEP-2000; 2000US-0229343.
PR   06-SEP-2000; 2000US-0230437.
PR   08-SEP-2000; 2000US-0231243.
PR   25-SEP-2000; 2000US-0234997.
PR   29-SEP-2000; 2000US-0236367.
PR   13-OCT-2000; 2000US-0239937.
PR   08-NOV-2000; 2000US-0246476.
PR   08-NOV-2000; 2000US-0246477.
PR   08-NOV-2000; 2000US-0246525.
PR   08-NOV-2000; 2000US-0246526.
PR   08-NOV-2000; 2000US-0246528.
PR   17-NOV-2000; 2000US-0249210.
PR   17-NOV-2000; 2000US-0249211.
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PR   17-NOV-2000; 2000US-0249214.
PR   17-NOV-2000; 2000US-0249265.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-476225/51.
XX
PT   Novel plasma membrane associated proteins useful for diagnosing,
PT   treating, preventing and/or prognosing disorders related to the
PT   proteins, including cancer, immune response and neuronal disorders
XX
PS   Example 2; SEQ ID NO 265; 532pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (AAI62752-AAI62961) and proteins
CC   (AAM42347-AAM42415) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC   in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC   and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC   epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC   and parasitic infections.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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SQ   Sequence 11617 BP; 3043 A; 2768 C; 2912 G; 2894 T; 0 other;


  Query Match             2.2%;  Score 22;  DB 22;  Length 11617;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
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Db    5191 atatatatacacacatatatac 5212


RESULT  45
AAV34455
ID   AAV34455 standard; DNA; 11722 BP.
XX
AC   AAV34455;
XX
DT   28-SEP-1998  (first entry)
XX
DE   Human MHC class I chain-related gene A (MICA).
XX
KW   MICA; MHC class I chain-related gene A; human;
KW   major histocompatibility complex; brain cancer; lymphatic cancer;
KW   liver cancer, stomach cancer; testicular cancer; cervical cancer;
KW   leukaemia; melanoma; head and neck cancer; oesophageal cancer;
KW   colon cancer; breast cancer; lung cancer; ovary cancer;
KW   prostate cancer; renal cancer; graft-versus-host disease;
KW   inflammatory bowel disease; adoptive immunotherapy; therapy;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             40..11548
FT                   /*tag= a
FT                   /note= "contains introns"
FT   exon            1..109
FT                   /*tag= b
FT                   /number= 1
FT   intron          110..6949
FT                   /*tag= c
FT                   /number= 1
FT   exon            6950..7204
FT                   /*tag= d
FT                   /number= 2
FT   intron          7205..7478
FT                   /*tag= e
FT                   /number= 2
FT   exon            7479..7766
FT                   /*tag= f
FT                   /number= 3
FT   intron          7767..8353
FT                   /*tag= g
FT                   /number= 3
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FT                   /*tag= h
FT                   /number= 4
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FT                   /number= 4
FT   exon            8732..8869
FT                   /*tag= j
FT                   /number= 5
FT   intron          8870..11420
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FT                   /number= 5
FT   exon            11421..11722
FT                   /*tag= l
FT                   /number= 6
XX
PN   WO9819167-A2.
XX
PD   07-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US020170.
XX
PR   29-OCT-1996;   96US-0029044.
XX
PA   (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI   Spies T.  Spies V;
XX
DR   WPI; 1998-272392/24.
DR   P-PSDB; AAW60043.
XX
PI   Use of MHC-related molecules, MICA and MICB - as targets for the
PI   detection and treatment of cancers and for isolating specific T cell
PI   populations which can be used for immunotherapy
XX
PS   Disclosure; Page 104-111; 125pp; English.
XX
CC   This is the human cell stress regulated MHC class I chain-related
CC   gene A (MICA).  It was obtained from single-stranded (M13) and
CC   double-stranded (pUC19) templates of mapped or randomly shot-gun
CC   subcloned DNA fragments that were derived from cosmid M32A.  The
CC   gene is located 40 kb centromeric of HLA-B.  It codes for a 385
CC   amino acid polypeptide (see AAW60043).  A cDNA clone (see AAV34456)
CC   coding for closely-related MICB (see AAW60044) is also provided.
CC   MICA and MICB are specifically expressed at the lining of the
CC   gastrointestinal tract, the primary site of infectious attack,
CC   and a major target for complications arising from graft-versus-host
CC   disease (GVHD).  They are also expressed at the cell surface of
```

CC colon and other cancer cells. A claimed method of detecting a
CC cancer cell involves identifying MICA or MICB in the sample. Also
CC claimed are methods of purifying, enriching and expanding V-delta 1
CC gamma-delta T (VT) cells using MICA or MICB polypeptides, a
CC method of adoptive immunotherapy using purified VT cells, a
CC method of increasing expression of MICA by providing a cell with
CC an expression construct comprising a MICA coding region under the
CC control of a promoter active in eukaryotic cells, and a transgenic
CC animal expressing MICA and/or MICB. A therapeutic agent (e.g.
CC a toxin or cytokine) conjugated to a MICA- or MICB-binding agent
CC (e.g. antibodies) can be used for the detection and treatment of
CC cancers such as brain cancer, lymphatic cancer, liver cancer,
CC stomach cancer, testicular cancer, cervical cancer, leukaemia,
CC melanoma, head and neck cancer, oesophageal cancer, colon cancer,
CC breast cancer, lung cancer, ovarian cancer, prostate cancer and
CC renal cancer (all claimed). The antibody can also be used in the
CC treatment of other disorders such as GVHD and inflammatory bowel
CC disease.
XX
SQ Sequence 11722 BP; 2414 A; 2996 C; 2828 G; 3484 T; 0 other;

Query Match 2.2%; Score 22; DB 19; Length 11722;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 gattgcattgaatctgtagatt 639
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Db 3518 gattgcattgaatctgtagatt 3539

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Searched: 351203 seqs, 113238999 residues

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Post-processing: Listing first 45 summaries

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SUMMARIES

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	3	23	4.0	3207	1	US-08-483-322-1	Sequence 1, Appli
	4	23	4.0	3207	2	US-08-478-882-1	Sequence 1, Appli
c	5	22	3.8	356	2	US-08-520-678A-22	Sequence 22, Appl
c	6	22	3.8	356	4	US-08-897-126-22	Sequence 22, Appl
	7	22	3.8	1731	1	US-08-203-905B-13	Sequence 13, Appl
	8	22	3.8	2010	1	US-07-864-475A-4	Sequence 4, Appli
	9	22	3.8	2010	2	US-08-468-249A-4	Sequence 4, Appli
c	10	22	3.8	8056	3	US-09-136-605-14	Sequence 14, Appl
c	11	22	3.8	8082	1	US-08-306-691B-41	Sequence 41, Appl
c	12	22	3.8	8082	1	US-08-187-785-1	Sequence 1, Appli
c	13	22	3.8	8082	5	PCT-US93-06251-28	Sequence 28, Appl
c	14	22	3.8	9646	3	US-08-811-566-1	Sequence 1, Appli
c	15	22	3.8	12980	3	US-08-811-566-5	Sequence 5, Appli
	16	21	3.7	157	1	US-08-153-051B-27	Sequence 27, Appl
	17	21	3.7	157	1	US-08-060-952C-43	Sequence 43, Appl
	18	21	3.7	157	2	US-08-151-477A-27	Sequence 27, Appl
	19	21	3.7	158	3	US-08-819-867-57	Sequence 57, Appl
	20	21	3.7	217	4	US-09-040-984-82	Sequence 82, Appl
	21	21	3.7	1423	4	US-08-916-576B-3	Sequence 3, Appli
	22	21	3.7	1821	4	US-09-056-105-23	Sequence 23, Appl
	23	21	3.7	2412	1	US-08-437-027-18	Sequence 18, Appl
	24	21	3.7	3111	3	US-08-891-845-1	Sequence 1, Appli
	25	20	3.5	339	2	US-08-619-542B-30	Sequence 30, Appl
c	26	20	3.5	413	4	US-09-328-111-25	Sequence 25, Appl
	27	20	3.5	744	1	US-08-036-555B-133	Sequence 133, App
	28	20	3.5	744	1	US-08-469-569-133	Sequence 133, App
	29	20	3.5	744	1	US-08-249-322A-133	Sequence 133, App
	30	20	3.5	744	1	US-08-468-526A-133	Sequence 133, App
	31	20	3.5	744	2	US-08-734-591A-133	Sequence 133, App
	32	20	3.5	744	2	US-08-469-660-133	Sequence 133, App
	33	20	3.5	744	3	US-08-341-018-1	Sequence 1, Appli
	34	20	3.5	744	3	US-08-470-335-133	Sequence 133, App
	35	20	3.5	744	4	US-08-735-021-133	Sequence 133, App
	36	20	3.5	744	4	US-08-734-664A-133	Sequence 133, App
	37	20	3.5	744	4	US-08-470-339-133	Sequence 133, App
	38	20	3.5	744	5	PCT-US94-05083C-129	Sequence 129, App
	39	20	3.5	744	5	PCT-US95-06846A-133	Sequence 133, App
	40	20	3.5	934	3	US-09-248-335-55	Sequence 55, Appl
	41	20	3.5	1192	1	US-08-380-916-2	Sequence 2, Appli
	42	20	3.5	1192	2	US-08-182-247-1	Sequence 1, Appli
	43	20	3.5	1192	3	US-08-721-690-2	Sequence 2, Appli
	44	20	3.5	1192	3	US-08-891-581-2	Sequence 2, Appli
	45	20	3.5	1802	4	US-09-032-523-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-09-040-984-27
; Sequence 27, Application US/09040984
; Patent No. 6210883
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Wang, TongTong
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
;   TITLE OF INVENTION: OF LUNG CANCER
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SEED and BERRY LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue
;     CITY: Seattle
;     STATE: WA
;     COUNTRY: USA
;     ZIP: 98104
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/040,984
;     FILING DATE: 18-MAR-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Maki, David J.
;     REGISTRATION NUMBER: 31,392
;     REFERENCE/DOCKET NUMBER: 210121.456
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 206-622-4900
;     TELEFAX: 206-282-6031
;     TELEX:
; INFORMATION FOR SEQ ID NO: 27:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 654 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-09-040-984-27


  Query Match           55.5%;  Score 319;  DB 4;  Length 654;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-129;
  Matches  319;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 acttgatataaaaaggatatccataatgaatatttatactgcatcctttacattagcca 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 ACTTGATATAAAAAGGATATCCATAATGAATATTTTATACTGCATCCTTTACATTAGCCA 147
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Qy      61 ctaaatacgttattgcttgatgaagacctttcacagaatcctatggattgcagcatttca 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 CTAAATACGTTATTGCTTGATGAAGACCTTTCACAGAATCCTATGGATTGCAGCATTTCA 207

Qy     121 cttggctacttcatacccatgccttaaagaggggcagtttctcaaaagcagaaacatgcc 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 CTTGGCTACTTCATACCCATGCCTTAAAGAGGGGCAGTTTCTCAAAAGCAGAAACATGCC 267

Qy     181 gccagttctcaagttttcctcctaactccatttgaatgtaagggcagctggccccccaatg 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 GCCAGTTCTCAAGTTTTCCTCCTAACTCCATTTGAATGTAAGGGCAGCTGGCCCCCCAATG 327

Qy     241 tggggaggtccgaacatttttctgaattcccatttttcttgttcgcggctaaatgacagttt 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 TGGGGAGGTCCGAACATTTTCTGAATTCCCATTTTCTTGTTCGCGGCTAAATGACAGTTT 387

Qy     301 ctgtcattacttagattcc 319
           ||||||||||||||||||
Db     388 CTGTCATTACTTAGATTCC 406


RESULT   2
US-07-946-497-1
; Sequence 1, Application US/07946497
; Patent No. 5506119
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,497
;      FILING DATE:  19921109
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3207 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  p-Meta-1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  113..1624
US-07-946-497-1


  Query Match             4.0%;  Score 23;  DB 1;  Length 3207;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     553 caaaaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||||
Db    3157 CAAAAAGGAAAAAAAAAAAAAAA 3179


RESULT   3
US-08-483-322-1
; Sequence 1, Application US/08483322
; Patent No. 5760178
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,322
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/946,497
;      FILING DATE:  09-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3207 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  p-Meta-1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  113..1624
US-08-483-322-1


  Query Match             4.0%;  Score 23;  DB 1;  Length 3207;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     553 caaaaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||||
Db    3157 CAAAAAGGAAAAAAAAAAAAAAA 3179


RESULT   4
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US-08-478-882-1
; Sequence 1, Application US/08478882
; Patent No. 5885575
;  GENERAL INFORMATION:
;     APPLICANT:  HERRLICH, Peter
;     APPLICANT:  PONTA, Helmut
;     APPLICANT:  GUENTHERT, Ursula
;     APPLICANT:  MATZKU, Siegfried
;     APPLICANT:  WENZL, Achim
;     TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;     TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;     TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington, D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/478,882
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/946,497
;       FILING DATE:  19921109
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  16915/145
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3207 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  p-Meta-1
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  113..1624
US-08-478-882-1


  Query Match             4.0%;  Score 23;  DB 2;  Length 3207;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     553 caaaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||||
Db    3157 CAAAAAGGAAAAAAAAAAAAAA 3179


RESULT   5
US-08-520-678A-22/c
; Sequence 22, Application US/08520678A
; Patent No. 5874565
;  GENERAL INFORMATION:
;     APPLICANT:  Rice, Charles M.
;     APPLICANT:  Kolykhalov, Alexander A.
;     TITLE OF INVENTION:  NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
;     TITLE OF INVENTION:  C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
;     NUMBER OF SEQUENCES:  39
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Howell & Haferkamp, L.C.
;       STREET:  7733 Forsyth Blvd., Suite 1400
;       CITY:  St. Louis
;       STATE:  MO
;       COUNTRY:  USA
;       ZIP:  63105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/520,678A
;       FILING DATE:
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Henderson, Melodie W.
;       REGISTRATION NUMBER:  37,848
;       REFERENCE/DOCKET NUMBER:  6029-6836
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  314-727-5188
;       TELEFAX:  314-727-6092
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  356 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-520-678A-22


  Query Match             3.8%;  Score 22;  DB 2;  Length 356;
  Best Local Similarity   100.0%;  Pred. No. 0.66;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||||
Db     203 AAAAAGGAAAAAAAAAAAAAA 182


RESULT   6
US-08-897-126-22/c
; Sequence 22, Application US/08897126
; Patent No. 6297003
;  GENERAL INFORMATION:
;     APPLICANT:  Rice, Charles M.
;     APPLICANT:  Kolykhalov, Alexander A.
;     TITLE OF INVENTION:  NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
;     TITLE OF INVENTION:  C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
;     NUMBER OF SEQUENCES:  39
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Howell & Haferkamp, L.C.
;       STREET:  7733 Forsyth Blvd., Suite 1400
;       CITY:  St. Louis
;       STATE:  MO
;       COUNTRY:  USA
;       ZIP:  63105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/897,126
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/520,678
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Henderson, Melodie W.
```

; REGISTRATION NUMBER: 37,848
; REFERENCE/DOCKET NUMBER: 6029-6836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-897-126-22

Query Match 3.8%; Score 22; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 554 aaaaaggaaaaaaaaaaaaaa 575
||||||||||||||||||||||
Db 203 AAAAAGGAAAAAAAAAAAAAA 182

RESULT 7
US-08-203-905B-13
; Sequence 13, Application US/08203905B
; Patent No. 5646249
; GENERAL INFORMATION:
; APPLICANT: KAYE, FEDERIC J.
; APPLICANT: OTTERSON, GREGORY A.
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: NOVEL CHAPERONE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,905B
; FILING DATE: February 28, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KIRKPATRICK, ANITA M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH089.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1731 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1730
US-08-203-905B-13

Query Match 3.8%; Score 22; DB 1; Length 1731;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 554 aaaaaggaaaaaaaaaaaaaa 575
||||||||||||||||||||||
Db 1606 AAAAAGGAAAAAAAAAAAAAA 1627

RESULT 8
US-07-864-475A-4
; Sequence 4, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2010
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-864-475A-4

Query Match 3.8%; Score 22; DB 1; Length 2010;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 554 aaaaaggaaaaaaaaaaaaaa 575
||||||||||||||||||||||
Db 1941 AAAAAGGAAAAAAAAAAAAAA 1962

RESULT 9
US-08-468-249A-4
; Sequence 4, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:

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;    APPLICANT:  Segre et al., Gino V.
;    TITLE OF INVENTION:  PARATHYROID HORMONE RECEPTOR AND DNA
;    TITLE OF INVENTION:  ENCODING SAME
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,249A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/864,475
;      FILING DATE:  06-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/681,702
;      FILING DATE:  04-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/071003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2010 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  28..1807
US-08-468-249A-4


  Query Match             3.8%;  Score 22;  DB 2;  Length 2010;
  Best Local Similarity   100.0%;  Pred. No. 0.58;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||||
Db    1941 AAAAAGGAAAAAAAAAAAAAAA 1962


RESULT  10
US-09-136-605-14/c
; Sequence 14, Application US/09136605A
; Patent No. 6140052
; GENERAL INFORMATION:
;  APPLICANT: He, Tong-Chuan
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Vogelstein, Bert
;  TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to
;  TITLE OF INVENTION: Prevent Cancer
;  FILE REFERENCE: 1107.75741
;  CURRENT APPLICATION NUMBER: US/09/136,605A
;  CURRENT FILING DATE: 1998-08-20
;  EARLIER APPLICATION NUMBER: 08/821,355
;  EARLIER FILING DATE: 1997-03-20
;  EARLIER APPLICATION NUMBER: 09/003,687
;  EARLIER FILING DATE: 1998-01-06
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 8056
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: TATA_signal
;   LOCATION: (2456)...(2462)
US-09-136-605-14


  Query Match             3.8%;  Score 22;  DB 3;  Length 8056;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||||
Db    6177 AAAAAGGAAAAAAAAAAAAAAA 6199


RESUL.  11
US-08-306-691B-41/c
; Sequence 41, Application US/08306691B
; Patent No. 5734039
;  GENERAL INFORMATION:
;    APPLICANT:  Calabretta, Bruno
;    APPLICANT:  Skorski, Tomasz
;    TITLE OF INVENTION:  ANTISENSE
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  Two Penn Center, Suite 1800
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 KB
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/306,691B
;      FILING DATE:  September 15, 1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5734039e
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8082 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-306-691B-41


  Query Match             3.8%;  Score 22;  DB 1;  Length 8082;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||||
Db    6146 AAAAAGGAAAAAAAAAAAAAAA 6225
```

```
RESULT 12
US-08-187-785-1/c
; Sequence 1, Application US/08187785
; Patent No. 5756476
;  GENERAL INFORMATION:
;     APPLICANT:  Epstein, Stephen
;     APPLICANT:  Unger, Ellis
;     APPLICANT:  Speir, Edith
;     TITLE OF INVENTION:  Inhibition of No. 5756476-Transformed Cell
;     TITLE OF INVENTION:  Proliferation Using Anti-Sense Oligonucleotides
;     NUMBER OF SEQUENCES:  13
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;       STREET:  620 Newport Center Dr.  Sixteenth Floor
;       CITY:  Newport Beach
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92660
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/187,785
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/821,415
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Altman, Daniel E.
;       REGISTRATION NUMBER:  34,115
;       REFERENCE/DOCKET NUMBER:  NIH001.001A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  714-760-0404
;       TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8082 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  Human
;     IMMEDIATE SOURCE:
;       CLONE:  C-Myc Genomic Clone
US-08-187-785-1


  Query Match             3.8%;  Score 22;  DB 1;  Length 8082;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||||
Db    6246 AAAAAGGAAAAAAAAAAAAAA 6225


RESULT 13
PCT-US93-06251-28/c
; Sequence 28, Application PC/TUS9306251
;  GENERAL INFORMATION:
;     APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;     TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;     TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;     NUMBER OF SEQUENCES:  93
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;       STREET:  400 Garden City Plaza
;       CITY:  Garden City
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  11530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/06251
;       FILING DATE:  19930630
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DiGiglio, Frank S.
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  8586
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  516-742-4343
;       TELEFAX:  516-742-4366
;       TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  28:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8082 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
PCT-US93-06251-28


  Query Match             3.8%;  Score 22;  DB 5;  Length 8082;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||||
Db    6246 AAAAAGGAAAAAAAAAAAAAA 6225


RESULT 14
US-08-811-566-1/c
; Sequence 1, Application US/08811566
; Patent No. 6127116
;  GENERAL INFORMATION:
;     APPLICANT:  Rice, Charles  et al.
;     TITLE OF INVENTION:  FUNCTIONAL DNA CLONE FOR HEPATITIS C
;     TITLE OF INVENTION:  VIRUS (HCV) AND USES THEREOF
;     NUMBER OF SEQUENCES:  21
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  David A. Jackson, Esq.
;       STREET:  411 Hackensack Ave, Continental Plaza, 4th
;       STREET:  Floor
;       CITY:  Hackensack
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/811,566
;       FILING DATE:  03-MAR-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jackson Esq., David A.
;       REGISTRATION NUMBER:  26,742
;       REFERENCE/DOCKET NUMBER:  1113-1-006
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-487-5800
```

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;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9646 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-811-566-1

  Query Match             3.8%;  Score 22;  DB 3;  Length 9646;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||||
Db    9493 AAAAAGGAAAAAAAAAAAAAA 9472


RESULT  15
US-08-811-566-5/c
; Sequence 5, Application US/08811566
; Patent No. 6127116
;  GENERAL INFORMATION:
;    APPLICANT:  Rice, Charles  et al.
;    TITLE OF INVENTION:  FUNCTIONAL DNA CLONE FOR HEPATITIS C
;    TITLE OF INVENTION:  VIRUS (HCV) AND USES THEREOF
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/811,566
;      FILING DATE:  03-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1113-1-006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12980 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-811-566-5

  Query Match             3.8%;  Score 22;  DB 3;  Length 12980;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     554 aaaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||||
Db    9495 AAAAAGGAAAAAAAAAAAAAA 9474


RESULT  16
US-08-153-051B-27
; Sequence 27, Application US/08153051B
; Patent No. 5645986
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine Strahl
;    APPLICANT:  Michael J. McEachern
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO TELOMERE
;    TITLE OF INVENTION:  LENGTH AND/OR TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 MB
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,051B
;      FILING DATE:  No. 5645986ember 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  204/195
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-153-051B-27

  Query Match             3.7%;  Score 21;  DB 1;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     555 aaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||||
Db     126 AAAAGGAAAAAAAAAAAAAA 146


RESULT  17
US-08-060-952C-43
; Sequence 43, Application US/08060952C
; Patent No. 5695932
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF CONDITIONS
;    TITLE OF INVENTION:  RELATED TO TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/060,952C
;      FILING DATE:  May 13, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/882,438
;      FILING DATE:  May 13, 1992
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/045
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-060-952C-43


  Query Match             3.7%;  Score 21;  DB 1;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     555 aaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     128 AAAAGGAAAAAAAAAAAAAAA 148


RESULT  18
US-08-151-477A-27
; Sequence 27, Application US/08151477A
; Patent No. 5830644
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine Strahl
;    APPLICANT:  Michael J. McEachern
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO TELOMERE
;    TITLE OF INVENTION:  LENGTH AND/OR TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 MB
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,477A
;      FILING DATE:  No. 5830644ember 12, 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/189
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-151-477A-27


  Query Match             3.7%;  Score 21;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     555 aaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     128 AAAAGGAAAAAAAAAAAAAAA 148


RESULT  19
US-08-819-867-57
; Sequence 57, Application US/08819867
; Patent No. 6007989
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Calvin B. Harley
;    APPLICANT:  Scott L. Weinrich
;    APPLICANT:  Catherine M. Strahl
;    APPLICANT:  Michael J. Mceachern
;    APPLICANT:  Jerry Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth H. Blackburn
;    APPLICANT:  Nam Woo Kim
;    APPLICANT:  Homayoun Vaziri
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF
;    TITLE OF INVENTION:  CONDITIONS RELATED TO
;    TITLE OF INVENTION:  TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
```

```
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  U.S.A.
;       ZIP:  90071-2066
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  FastSEQ for Windows 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/819,867
;       FILING DATE:  March 14, 1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/153,051
;       FILING DATE:  No. 6007989ember 12, 1993
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Chambers, Daniel M.
;       REGISTRATION NUMBER:  34,561
;       REFERENCE/DOCKET NUMBER:  224/232
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  57:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  158 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-819-867-57


  Query Match             3.7%;  Score 21;  DB 3;  Length 158;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     555 aaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     128 AAAAGGAAAAAAAAAAAAAAA 148


RESULT  20
US-09-040-984-82
; Sequence 82, Application US/09040984
; Patent No. 6210883
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Wang, TongTong
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR DIAGNOSIS
;    TITLE OF INVENTION:  OF LUNG CANCER
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/040,984
;      FILING DATE:  18-MAR-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.456
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-282-6031
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  217 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-040-984-82


  Query Match             3.7%;  Score 21;  DB 4;  Length 217;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     555 aaaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     190 AAAAGGAAAAAAAAAAAAAAA 210


RESULT  21
US-08-916-576B-3
; Sequence 3, Application US/08916576B
; Patent No. 6171815
;  GENERAL INFORMATION:
;    APPLICANT:  YU, GUO-LIANG
;    APPLICANT:  DILLON, PATRICK J.
;    APPLICANT:  EBNER, REINHARD
;    APPLICANT:  ENDRESS, GREGORY A.
;    TITLE OF INVENTION:  NOVEL HUMAN GROWTH FACTORS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/916,576B
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/024,347
;      FILING DATE:  23-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0500001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1423 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  88..603
;    FEATURE:
;      NAME/KEY:  mat_peptide
```

; LOCATION: 157..603
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 88..156
US-08-916-576B-3

Query Match 3.7%; Score 21; DB 4; Length 1423;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 555 aaaaggaaaaaaaaaaaaaaa 575
||||||||||||||||||||||
Db 1400 AAAAGGAAAAAAAAAAAAAAA 1420

RESULT 22
US-09-056-105-23
; Sequence 23, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-23

Query Match 3.7%; Score 21; DB 4; Length 1821;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 555 aaaaggaaaaaaaaaaaaaaa 575
||||||||||||||||||||||
Db 932 aaaaggaaaaaaaaaaaaaaa 952

RESULT 23
US-08-437-027-18
; Sequence 18, Application US/08437027
; Patent No. 5670317
; GENERAL INFORMATION:
; APPLICANT: Landanyi, Marc
; APPLICANT: Gerald, William
; TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
; TITLE OF INVENTION: SMALL ROUND CELL TUMOR
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,027
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 46416/JPW/CCA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-437-027-18

Query Match 3.7%; Score 21; DB 1; Length 2412;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 555 aaaaggaaaaaaaaaaaaaaa 575
||||||||||||||||||||||
Db 2391 AAAAGGAAAAAAAAAAAAAAA 2411

RESULT 24
US-08-891-845-1
; Sequence 1, Application US/08891845
; Patent No. 6056873
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; APPLICANT: Sliwkowski, Mark
; TITLE OF INVENTION: Gamma-Heregulin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3111 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-891-845-1

Query Match 3.7%; Score 21; DB 3; Length 3111;

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  Best Local Similarity   100.0%;  Pred. No. 1.5:
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     555 aaaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||
Db    3091 AAAAGGAAAAAAAAAAAAAAA 3111


RESULT  25
US-08-619-542B-30
; Sequence 30, Application US/08619542B
; Patent No. 5830662
;  GENERAL INFORMATION:
;    APPLICANT:  The Trustees of Columbia University in the City
;    APPLICANT:  of New York
;    TITLE OF INVENTION:  METHOD FOR CONSTRUCTION OF NORMALIZED
;    TITLE OF INVENTION:  cDNA LIBRARIES
;    NUMBER OF SEQUENCES:  78
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/619,542B
;      FILING DATE:  June 21, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  42840-A-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  339 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-619-542B-30


  Query Match             3.5%;  Score 20;  DB 2;  Length 339;
  Best Local Similarity   100.0%;  Pred. No. 4.8:
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||
Db     317 AAAGGAAAAAAAAAAAAAAA 336


RESULT  26
US-09-328-111-25/c
; Sequence 25, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,601
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 413
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-328-111-25


  Query Match             3.5%;  Score 20;  DB 4;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 4.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           |||||||||||||||||||||
Db      39 AAAGGAAAAAAAAAAAAAAA 20


RESULT  27
US-08-036-555B-133
; Sequence 133, Application US/08036555B
; Patent No. 5530109
;  GENERAL INFORMATION:
;    APPLICANT:  Goodearl, Andrew; Strobant, Paul;
;    APPLICANT:  Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
;    APPLICANT:  Chen, Maio Su; Hiles, Ian
;    TITLE OF INVENTION:  Glial Mitogenic Factors, Their
;    TITLE OF INVENTION:  Preparation and Use
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/036,555B
;      FILING DATE:  24-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  30-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APRIL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.K. 91 07566.3
;      FILING DATE:  10-APRIL-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Tsai, Christine H.
;      REGISTRATION NUMBER:  34,266
;      REFERENCE/DOCKET NUMBER:  LUD 5250.4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  133:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-036-555B-133


  Query Match             3.5%;  Score 20;  DB 1;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  28
US-08-469-569-133
; Sequence 133, Application US/08469569
; Patent No. 5606032
;  GENERAL INFORMATION:
;    APPLICANT:  Goodearl, Andrew; Stroobant, Paul;
;    APPLICANT:  Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
;    APPLICANT:  Chen, Maio Su; Hiles, Ian
;    TITLE OF INVENTION:  Glial Mitogenic Factors, Their
;    TITLE OF INVENTION:  Preparation and Use
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,569
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/036,555
;      FILING DATE:  24-MAR-1993
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  30-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APRIL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.K. 91 07566.3
;      FILING DATE:  10-APRIL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsai, Christine H.
;      REGISTRATION NUMBER:  34,266
;      REFERENCE/DOCKET NUMBER:  LUD 5250.4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  133:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-469-569-133


  Query Match             3.5%;  Score 20;  DB 1;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  29
US-08-249-322A-133
; Sequence 133, Application US/08249322A
; Patent No. 5716930
;  GENERAL INFORMATION:
;    APPLICANT:  Goodearl, Andrew; Stroobant, Paul;
;    APPLICANT:  Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
;    APPLICANT:  Chen, Maio Su; Hiles, Ian
;    TITLE OF INVENTION:  Glial Mitogenic Factors, Their
;    TITLE OF INVENTION:  Preparation and Use
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/249,322A
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/036,555
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  30-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APRIL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.K. 91 07566.3
;      FILING DATE:  10-APRIL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsai, Christine H.
;      REGISTRATION NUMBER:  34,266
;      REFERENCE/DOCKET NUMBER:  LUD 250.4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  133:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-249-322A-133


  Query Match             3.5%;  Score 20;  DB 1;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  30
US-08-469-526A-133
; Sequence 133, Application US/08469526A
; Patent No. 5792849
;  GENERAL INFORMATION:
;    APPLICANT:  Goodearl, Andrew
;    APPLICANT:  Stroobant, Paul
;    APPLICANT:  Minghetti, Luisa
;    APPLICANT:  Waterfield, Michael
;    APPLICANT:  Marchionni, Mark
;    APPLICANT:  Chen, Maio Su
;    APPLICANT:  Hiles, Ian
;    TITLE OF INVENTION:  GLIAL MITOGENIC FACTORS, THEIR
;    TITLE OF INVENTION:  PREPARATION AND USE
;    NUMBER OF SEQUENCES:  187
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,526A
;      FILING DATE:  06 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/036,555
;      FILING DATE:  24-MAR-1993
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  03-JUN-1992
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APRIL-1992
;      APPLICATION NUMBER:  U.K. 91 07566.3
;      FILING DATE:  10-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bieker-Brady, Kristina
;      REGISTRATION NUMBER:  39,109
;      REFERENCE/DOCKET NUMBER:  04585/00200A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;  INFORMATION FOR SEQ ID NO:  133:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-469-526A-133


  Query Match             3.5%;  Score 20;  DB 1;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  31
US-08-734-591A-133
; Sequence 133, Application US/08734591A
; Patent No. 5854220
;  GENERAL INFORMATION:
;    APPLICANT:  Goodearl, Andrew
;    APPLICANT:  Stroobant, Paul
;    APPLICANT:  Minghetti, Luisa
;    APPLICANT:  Waterfield, Michael
;    APPLICANT:  Hiles, Ian
;    APPLICANT:  Marchionni, Mark
;    APPLICANT:  Chen, Mario
;    TITLE OF INVENTION:  GLIAL MITOGENIC FACTORS, THEIR
;    TITLE OF INVENTION:  PREPARATION AND USE
;    NUMBER OF SEQUENCES:  187
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 MB
;      COMPUTER:  IBM Compatible Pentium
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  WordPerfect (Version 7.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/734,591A
;      FILING DATE:  22-OCT-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/470,335
;      FILING DATE:  06-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/036,555
;      FILING DATE:  03-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  30-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 91 07566.3
;      FILING DATE:  10-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bieker-Brady, Kristina
;      REGISTRATION NUMBER:  39,109
;      REFERENCE/DOCKET NUMBER:  04585/00200P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 428-0200
;      TELEFAX:  (617) 428-7045
;      TELEX:
```

```
;  INFORMATION FOR SEQ ID NO:  133:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-734-591A-133


  Query Match             3.5%;  Score 20;  DB 2;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  32
US-08-469-660-133
; Sequence 133, Application US/08469660
; Patent No. 5876973
;  GENERAL INFORMATION:
;    APPLICANT:  Gwynne, David I.; Marchionni, Mark;
;    APPLICANT:  McBurney, Robert N.
;    TITLE OF INVENTION:  INHIBITORS OF CELL PROLIFERATION,
;    TITLE OF INVENTION:  THEIR PREPARATION AND USE
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      ZIP:  0211-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,660
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/011,396
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/984,085
;      FILING DATE:  01-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/951,747
;      FILING DATE:  25-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/927,337
;      FILING DATE:  10-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  04585/017004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  200154
;  INFORMATION FOR SEQ ID NO:  133:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-469-660-133


  Query Match             3.5%;  Score 20;  DB 2;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  33
US-08-341-018-1
; Sequence 1, Application US/08341018A
; Patent No. 6087323
; GENERAL INFORMATION:
;  APPLICANT: Gywnne, David I.
;  APPLICANT: Mahanthappa, Nagesh K.
;  APPLICANT: Marchionni, Mark A.
;  APPLICANT: Bermingham-McDonogh, Olivia
;  APPLICANT: Goldin, Stanley M.
;  APPLICANT: McBurney, Robert N.
;  TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF
;  TITLE OF INVENTION: CELLULAR COMMUNICATION
;  FILE REFERENCE: 04585/041001
;  CURRENT APPLICATION NUMBER: US/08/341,018A
;  CURRENT FILING DATE: 1994-11-17
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8)...(625)
US-08-341-018-1


  Query Match             3.5%;  Score 20;  DB 3;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 aaaggaaaaaaaaaaaaaaa 694


RESULT  34
US-08-470-335-133
; Sequence 133, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
;  APPLICANT: GOODEARL, ANDREW
;  APPLICANT: STROOBANT, PAUL
;  APPLICANT: MINGHETTI, LUISA
;  APPLICANT: WATERFIELD, MICHAEL
;  APPLICANT: MARCHIONNI, MARK
;  APPLICANT: CHEN, MARIO S.
;  APPLICANT: HILES, IAN
;  TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
;  TITLE OF INVENTION: PREPARATION AND USE
;  FILE REFERENCE: 04585/00200B
;  CURRENT APPLICATION NUMBER: US/08/470,335F
;  CURRENT FILING DATE: 1995-06-06
;  EARLIER APPLICATION NUMBER: 08/036,555
;  EARLIER FILING DATE: 1993-03-24
;  NUMBER OF SEQ ID NOS: 252
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8)...(625)
US-08-470-335-133
```

```
  Query Match             3.5%;  Score 20;  DB 3;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 aaaggaaaaaaaaaaaaaaa 694


RESULT  35
US-08-735-021-133
; Sequence 133, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
;  APPLICANT: GOODEARL, ANDREW
;  APPLICANT: STROOBANT, PAUL
;  APPLICANT: MINGHETTI, LUISA
;  APPLICANT: WATERFIELD, MICHAEL
;  APPLICANT: MARCHIONNI, MARK
;  APPLICANT: CHEN, MARIO S.
;  APPLICANT: HILES, IAN
;  TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
;  TITLE OF INVENTION: PREPARATION AND USE
;  FILE REFERENCE: 04585/00200L
;  CURRENT APPLICATION NUMBER: US/08/735,021B
;  CURRENT FILING DATE: 1996-10-22
;  EARLIER APPLICATION NUMBER: 08/472,065
;  EARLIER FILING DATE: 1995-06-06
;  EARLIER APPLICATION NUMBER: 08/036,555
;  EARLIER FILING DATE: 1993-03-24
;  EARLIER APPLICATION NUMBER: 07/965,173
;  EARLIER FILING DATE: 1992-10-23
;  EARLIER APPLICATION NUMBER: 07/940,389
;  EARLIER FILING DATE: 1992-09-03
;  EARLIER APPLICATION NUMBER: 07/907,138
;  EARLIER FILING DATE: 1992-06-30
;  EARLIER APPLICATION NUMBER: 07/863,703
;  EARLIER FILING DATE: 1992-04-03
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8)...(625)
US-08-735-021-133


  Query Match             3.5%;  Score 20;  DB 4;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 aaaggaaaaaaaaaaaaaaa 694


RESULT  36
US-08-734-664A-133
; Sequence 133, Application US/08734664A
; Patent No. 6204241
;  GENERAL INFORMATION:
;     APPLICANT:  Goodearl, Andrew
;     APPLICANT:  Stroobant, Paul
;     APPLICANT:  Minghetti, Luisa
;     APPLICANT:  Waterfield, Michael
;     APPLICANT:  Marchionni, Mark
;     APPLICANT:  Chen, Mario
;     APPLICANT:  Hiles, Ian
;     TITLE OF INVENTION:  GLIAL MITOGENIC FACTORS, THEIR
;     TITLE OF INVENTION:  PREPARATION AND USE
;     NUMBER OF SEQUENCES:  187
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Clark & Elbing LLP
;       STREET:  176 Federal Street
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  U.S.A.
;       ZIP:  02110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 MB
;       COMPUTER:  IBM Compatible Pentium
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSeq Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/734,664A
;       FILING DATE:  22-OCT-1996
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/249,322
;       FILING DATE:  26-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/036,555
;       FILING DATE:  24-MAR-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/965,173
;       FILING DATE:  23-OCT-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/940,389
;       FILING DATE:  03-SEP-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/907,138
;       FILING DATE:  30-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/863,703
;       FILING DATE:  03-APR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  UK 91 07566.3
;       FILING DATE:  10-APR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bieker-Brady, Kristina
;       REGISTRATION NUMBER:  39,109
;       REFERENCE/DOCKET NUMBER:  04585/002d0J
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 428-0200
;       TELEFAX:  (617) 428-7045
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  133:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  744
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-734-664A-133


  Query Match             3.5%;  Score 20;  DB 4;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  37
US-08-470-339-133
; Sequence 133, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
;  APPLICANT: GOODEARL, ANDREW
;  APPLICANT: STROOBANT, PAUL
```

```
;  APPLICANT: MINGHETTI, LUISA
;  APPLICANT: WATERFIELD, MICHAEL
;  APPLICANT: MARCHIONNI, MARK
;  APPLICANT: CHEN, MARIO S.
;  APPLICANT: HILES, IAN
;  TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
;  TITLE OF INVENTION: PREPARATION AND USE
;  FILE REFERENCE: 04585/002008
;  CURRENT APPLICATION NUMBER: US/08/470,339C
;  CURRENT FILING DATE: 1995-06-06
;  EARLIER APPLICATION NUMBER: 08/036,555
;  EARLIER FILING DATE: 1993-03-24
;  EARLIER APPLICATION NUMBER: 07/940,389
;  EARLIER FILING DATE: 1992-09-03
;  EARLIER APPLICATION NUMBER: 07/907,138
;  EARLIER FILING DATE: 1992-06-30
;  EARLIER APPLICATION NUMBER: 07/863,703
;  EARLIER FILING DATE: 1992-04-03
;  EARLIER APPLICATION NUMBER: 91 07566.3 GB
;  EARLIER FILING DATE: 1999-04-10
;  NUMBER OF SEQ ID NOS: 226
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;    LENGTH: 744
;    TYPE: DNA
;    ORGANISM: Bos taurus
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (8)...(625)
US-08-470-339-133


  Query Match             3.5%;  Score 20;  DB 4;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 aaaggaaaaaaaaaaaaaa 694


RESULT  38
PCT-US94-05083C-129
; Sequence 129, Application PC/TUS94050830
;  GENERAL INFORMATION:
;    APPLICANT:  Robert Sklar, Mark Marchionni,
;    APPLICANT:  David I. Gwynne
;    TITLE OF INVENTION:  METHODS FOR ALTERING
;    TITLE OF INVENTION:  MUSCLE CONDITION
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360
;      MEDIUM TYPE:  kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05083C
;      FILING DATE:  06-MAY-94
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/209,204
;      FILING DATE:  08-MAR-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/059,022
;      FILING DATE:  06-May-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  04585/026WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  129:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US94-05083C-129


  Query Match             3.5%;  Score 20;  DB 5;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  39
PCT-US95-06846A-133
; Sequence 133, Application PC/TUS9506846A
;  GENERAL INFORMATION:
;    APPLICANT:  Goodearl, Andrew David; Strobant, Paul;
;    APPLICANT:  Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
;    APPLICANT:  Chen, Maio Su; Hiles, Ian
;    TITLE OF INVENTION:  Glial Mitogenic Factors, Their
;    TITLE OF INVENTION:  Preparation and Use
;    NUMBER OF SEQUENCES:  178
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06846A
;      FILING DATE:  25-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/249,322
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/036,555
;      FILING DATE:  24-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  30-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APRIL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.K. 91 07566.3
;      FILING DATE:  10-APRIL-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Hanson, Norman D.
;       REGISTRATION NUMBER:  30,946 .
;       REFERENCE/DOCKET NUMBER:  LUD.5250.5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 688-9200
;       TELEFAX:  (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  133:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  744
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
PCT-US95-06846A-133


  Query Match             3.5%;  Score 20;  DB 5;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     675 AAAGGAAAAAAAAAAAAAAA 694


RESULT  40
US-09-248-335-55
; Sequence 55, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
;  APPLICANT: MCGONIGLE, BRIAN
;  APPLICANT: O'KEEF, DANIEL
;  TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
;  FILE REFERENCE: CL-1128-A
;  CURRENT APPLICATION NUMBER: US/09/248,335
;  CURRENT FILING DATE: 1999-02-10
;  EARLIER APPLICATION NUMBER: 08/924,759
;  EARLIER FILING DATE: 1997-September-05
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 55
;   LENGTH: 934
;   TYPE: DNA
;   ORGANISM: maize
US-09-248-335-55


  Query Match             3.5%;  Score 20;  DB 3;  Length 934;
  Best Local Similarity   100.0%;  Pred. No. 4.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     912 aaaggaaaaaaaaaaaaaaa 931


RESULT  41
US-08-380-916-2
; Sequence 2, Application US/08380916
; Patent No. 5648478
;  GENERAL INFORMATION:
;    APPLICANT:  Calydon, Inc.
;    TITLE OF INVENTION:  Tissue-Specific Enhancer Active in
;    TITLE OF INVENTION:  Prostrate
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcardero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/380,916
;      FILING DATE:  12-JAN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/182,247
;      FILING DATE:  13-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I.
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  FP-60058-PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1192 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-380-916-2


  Query Match             3.5%;  Score 20;  DB 1;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     177 AAAGGAAAAAAAAAAAAAAA 196


RESULT  42
US-08-182-247-1
; Sequence 1, Application US/08182247
; Patent No. 5830686
;  GENERAL INFORMATION:
;    APPLICANT:  HENDERSON, DANIEL R
;    TITLE OF INVENTION:  TISSUE-SPECIFIC ENHANCER ACTIVE IN
;    TITLE OF INVENTION:  PROSTATE
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/182,247
;      FILING DATE:  13-JAN-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  16434-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1192 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  PROSTATE
US-08-182-247-1


  Query Match             3.5%;  Score 20;  DB 2;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
           ||||||||||||||||||||
Db     177 AAAGGAAAAAAAAAAAAAAA 196


RESULT  43
US-08-721-690-2
; Sequence 2, Application US/08721690
; Patent No. 6057299
;  GENERAL INFORMATION:
;    APPLICANT:  Henderson, Daniel R.
;    TITLE OF INVENTION:  TISSUE-SPECIFIC ENHANCER ACTIVE
;    TITLE OF INVENTION:  IN PROSTATE
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/721,690
;      FILING DATE:  27-SEP-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/380,916
;      FILING DATE:  30-JAN-1995
;      APPLICATION NUMBER:  US 08/182,247
;      FILING DATE:  13-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Catherine, Polizzi M
;      REGISTRATION NUMBER:  40,130
;      REFERENCE/DOCKET NUMBER:  34802-20001.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1192 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-08-721-690-2


  Query Match             3.5%;  Score 20;  DB 3;  Length 1192;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     556 aaaggaaaaaaaaaaaaaaa 575
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Db     177 AAAGGAAAAAAAAAAAAAAA 196


RESULT  44
US-08-891-581-2
; Sequence 2, Application US/08891581
; Patent No. 6136792
;  GENERAL INFORMATION:
;    APPLICANT:  Henderson, Daniel R.
;    TITLE OF INVENTION:  TISSUE SPECIFIC ENHANCER ACTIVE
;    TITLE OF INVENTION:  IN PROSTATE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/891,581
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/380,916
;      FILING DATE:  30-JAN-1995
;      APPLICATION NUMBER:  US 08/182,247
;      FILING DATE:  13-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Catherine, Polizzi M
;      REGISTRATION NUMBER:  40,130
;      REFERENCE/DOCKET NUMBER:  34802-20001.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1192 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-08-891-581-2


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Db     177 AAAGGAAAAAAAAAAAAAAA 196


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; Sequence 5, Application US/09032523
; Patent No. 6232454
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Guegler, Karl
;    APPLICANT:  Baugh, Mariah
;    TITLE OF INVENTION:  HUMAN PROTEINASE MOLECULES
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
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;       STREET:  3174 Porter Drive
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/032,523
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0479 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-855-0555
;       TELEFAX:  650-845-4166
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1802 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-032-523-5


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Db    1758 AAAGGAAAAAAAAAAAAAAA 1777


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Job time: 10918 sec
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RESULT 8
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AC AAV34234;
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DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein gene 16 clone HMABH07.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839446-A2.
XX
PD 11-SEP-1998.
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PF 06-MAR-1998; 98WO-US04492.
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PR 07-MAR-1997; 97US-0038621.
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PR 23-MAY-1997; 97US-0047600.
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PR 23-MAY-1997; 97US-0047613.
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PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
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PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.

PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
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PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
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PR 22-AUG-1997; 97US-0056886.
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PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Graves KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
DR WPI; 1998-609887/51.
DR P-PSDB; AAW75137.
XX
PT New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 234; 447pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34145) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).
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SQ Sequence 1053 BP; 248 A; 298 C; 295 G; 209 T; 3 other;

Query Match 3.7%; Score 22; DB 19; Length 1053;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1014 catatttaaaaaaaaaaaaaa 1035

GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 351203 seqs, 113238999 residues

Word size : 10

Total number of hits satisfying chosen parameters: 77163

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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c	2	21	2.3	4576	2	US-08-832-877-49	Sequence 49, Appl
c	3	20	2.2	588	4	US-09-385-982-275	Sequence 275, App
c	4	20	2.2	3226	3	US-08-870-126-10	Sequence 10, Appl
c	5	20	2.2	152331	3	US-09-128-155-16	Sequence 16, Appl
c	6	20	2.2	176373	3	US-09-128-155-17	Sequence 17, Appl
	7	19	2.1	28	2	US-08-858-767-21	Sequence 21, Appl
	8	19	2.1	28	2	US-08-858-767-22	Sequence 22, Appl
	9	19	2.1	28	2	US-08-858-767-23	Sequence 23, Appl
	10	19	2.1	28	2	US-08-863-028-21	Sequence 21, Appl
	11	19	2.1	28	2	US-08-863-028-22	Sequence 22, Appl
	12	19	2.1	28	2	US-08-863-028-23	Sequence 23, Appl
	13	19	2.1	1134	3	US-09-248-335-29	Sequence 29, Appl
	14	19	2.1	1235	3	US-08-672-650-5	Sequence 5, Appli
	15	19	2.1	2209	1	US-08-514-014-1	Sequence 1, Appli
	16	19	2.1	2209	2	US-08-633-823-1	Sequence 1, Appli
	17	19	2.1	2280	3	US-08-813-150-1	Sequence 1, Appli
	18	19	2.1	3171	5	PCT-US95-09261-1	Sequence 1, Appli
c	19	19	2.1	6143	1	US-08-612-521-3	Sequence 3, Appli
	20	18	1.9	53	4	US-09-091-332A-50	Sequence 50, Appl
	21	18	1.9	57	1	US-08-120-827-85	Sequence 85, Appl
	22	18	1.9	57	1	US-08-478-675-85	Sequence 85, Appl
	23	18	1.9	308	2	US-08-721-488-4	Sequence 4, Appli
	24	18	1.9	343	4	US-08-943-731-157	Sequence 157, App
	25	18	1.9	413	4	US-09-342-653-1	Sequence 1, Appli
	26	18	1.9	429	1	US-08-686-876A-13	Sequence 13, Appl
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c	28	18	1.9	432	2	US-08-858-830-1	Sequence 1, Appli
c	29	18	1.9	432	2	US-08-858-834-1	Sequence 1, Appli
	30	18	1.9	581	1	US-08-578-649-4	Sequence 4, Appli
c	31	18	1.9	582	4	US-09-385-982-98	Sequence 98, Appl
c	32	18	1.9	621	4	US-09-328-111-572	Sequence 572, App
	33	18	1.9	750	4	US-09-461-474-13	Sequence 13, Appl
	34	18	1.9	854	1	US-08-684-672-25	Sequence 25, Appl
	35	18	1.9	854	1	US-08-684-672-26	Sequence 26, Appl
	36	18	1.9	1305	2	US-08-866-410-37	Sequence 37, Appl
	37	18	1.9	1333	4	US-09-073-297-1	Sequence 1, Appli
	38	18	1.9	1338	1	US-08-631-200-14	Sequence 14, Appl
	39	18	1.9	1338	1	US-08-829-553-14	Sequence 14, Appl
	40	18	1.9	1338	2	US-08-922-267A-14	Sequence 14, Appl
	41	18	1.9	1338	2	US-08-936-707A-14	Sequence 14, Appl
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	43	18	1.9	1338	3	US-09-248-203-14	Sequence 14, Appl
	44	18	1.9	1338	4	US-09-406-071-14	Sequence 14, Appl
	45	18	1.9	1338	4	US-08-955-918C-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-08-832-883-49/c
; Sequence 49, Application US/08832883
; Patent No. 5807681
;  GENERAL INFORMATION:
;    APPLICANT:  Giordano, Antonio
;    APPLICANT:  Baldi, Alphonso
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS AND PROGNOSIS
;    TITLE OF INVENTION:  OF CANCER
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
;      STREET:  Suite 1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,883
;      FILING DATE:  4.4.97
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-13 US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4576 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-832-883-49
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Query Match 2.3%; Score 21; DB 1; Length 4576;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT   2
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; Sequence 49, Application US/08832877
; Patent No. 5840506
;  GENERAL INFORMATION:
;    APPLICANT:  Giordano, Antonio
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  116
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
;      STREET:  Suite 1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,877
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-13 US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4576 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-832-877-49

  Query Match             2.3%;  Score 21;  DB 2;  Length 4576;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    2859 GAAGGCAAAAAAAAAAAAAAA 2839


RESULT   3
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; Sequence 275, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
;  APPLICANT: ENDEGE, WILSON O., ET AL.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS:  II
;  FILE REFERENCE: CCDNA-260XX
;  CURRENT APPLICATION NUMBER: US/09/385,982
;  CURRENT FILING DATE: 1999-08-30
;  EARLIER APPLICATION NUMBER: 09/328,111
;  EARLIER FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: 60/117,393
;  EARLIER FILING DATE: 1999-01-27
;  EARLIER APPLICATION NUMBER: 60/098,639
;  EARLIER FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 544
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 275
;    LENGTH: 588
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(588)
;    OTHER INFORMATION: n = A,T,C or G
US-09-385-982-275

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  Best Local Similarity   100.0%;  Pred. No. 4.6;
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; Patent No. 6048702
;  GENERAL INFORMATION:
;    APPLICANT:  Prendergast, George C.
;    APPLICANT:  Sakamuro, Daitoku
;    TITLE OF INVENTION:  Murine and Human Box-Dependent
;    TITLE OF INVENTION:  MYC-Interacting Protein (Bin1) and Uses Therefor
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, P O Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/870,126
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/435,454
;      FILING DATE:  05-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,972
;      FILING DATE:  24-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kodroff, Cathy A.
;      REGISTRATION NUMBER:  33,980
;      REFERENCE/DOCKET NUMBER:  WST60CUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3226 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  677..734
;      OTHER INFORMATION:  /note= "exon 3"
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  851..945
;      OTHER INFORMATION:  /note= "exon 4"
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;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1408..1503
;      OTHER INFORMATION:  /note= "exon 5"
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2473..2579
;      OTHER INFORMATION:  /note= "exon 6"
US-08-870-126-10

  Query Match              2.2%;  Score 20;  DB 3;  Length 3226;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     262 ttctcagagcctcagtttcc 281
           ||||||||||||||||||||
Db    1297 TTCTCAGAGCCTCAGTTTCC 1278


RESULT   5
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

  Query Match              2.2%;  Score 20;  DB 3;  Length 152331;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     905 aaggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||||
Db    8501 AAGGCAAAAAAAAAAAAAAA 8482


RESULT   6
US-09-128-155-17/c
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELAIED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 176373
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(176373)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

  Query Match              2.2%;  Score 20;  DB 3;  Length 176373;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     905 aaggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||||
Db   93713 AAGGCAAAAAAAAAAAAAAA 93694


RESULT   7
US-08-858-767-21
; Sequence 21, Application US/08858767
; Patent No. 5837468
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, Xun
;    APPLICANT:  DUVICK, Jonathan P.
;    APPLICANT:  BRIGGS, Steven P.
;    TITLE OF INVENTION:  PCR-BASED CDNA SUBTRACTIVE CLONING
;    TITLE OF INVENTION:  METHOD
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,767
;      FILING DATE:  19-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,687
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/325/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-858-767-21

  Query Match              2.1%;  Score 19;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
```

```
                    ||||||||||||||||||||
Db      7 AGGCAAAAAAAAAAAAAAA 25


RESULT   8
US-08-858-767-22
; Sequence 22, Application US/08858767
; Patent No. 5837468
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, Xun
;    APPLICANT:  DUVICK, Jonathan P.
;    APPLICANT:  BRIGGS, Steven P.
;    TITLE OF INVENTION:  PCR-BASED CDNA SUBTRACTIVE CLONING
;    TITLE OF INVENTION:  METHOD
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,767
;      FILING DATE:  19-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,687
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/325/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-858-767-22


  Query Match             2.1%;  Score 19;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
           |||||||||||||||||||
Db       7 AGGCAAAAAAAAAAAAAAA 25


RESULT   9
US-08-858-767-23
; Sequence 23, Application US/08858767
; Patent No. 5837468
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, Xun
;    APPLICANT:  DUVICK, Jonathan P.
;    APPLICANT:  BRIGGS, Steven P.
;    TITLE OF INVENTION:  PCR-BASED CDNA SUBTRACTIVE CLONING
;    TITLE OF INVENTION:  METHOD
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,767
;      FILING DATE:  19-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,687
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  33229/325/PIHI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-858-767-23


  Query Match             2.1%;  Score 19;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
           |||||||||||||||||||
Db       7 AGGCAAAAAAAAAAAAAAA 25


RESULT   10
US-08-863-028-21
; Sequence 21, Application US/08863028
; Patent No. 5859991
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, Xun
;    APPLICANT:  DUVICK, Jonathan P.
;    APPLICANT:  BRIGGS, Steven P.
;    TITLE OF INVENTION:  PCR-BASED CDNA SUBTRACTIVE CLONING
;    TITLE OF INVENTION:  METHOD
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,028
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,767
;      FILING DATE:  19-MAY-1997
```

; APPLICATION NUMBER: US 08/481,687
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/325/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-863-028-21

Query Match 2.1%; Score 19; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 906 aggcaaaaaaaaaaaaaaa 924
||||||||||||||||||||
Db 7 AGGCAAAAAAAAAAAAAAA 25

RESULT 11
US-08-863-028-22
; Sequence 22, Application US/08863028
; Patent No. 5853991
; GENERAL INFORMATION:
; APPLICANT: WANG, Xun
; APPLICANT: DUVICK, Jonathan P.
; APPLICANT: BRIGGS, Steven P.
; TITLE OF INVENTION: PCR-BASED CDNA SUBTRACTIVE CLONING
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,028
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,767
; FILING DATE: 19-MAY-1997
; APPLICATION NUMBER: US 08/481,687
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/325/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-863-028-22

Query Match 2.1%; Score 19; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 906 aggcaaaaaaaaaaaaaaa 924
||||||||||||||||||||
Db 7 AGGCAAAAAAAAAAAAAAA 25

RESULT 12
US-08-863-028-23
; Sequence 23, Application US/08863028
; Patent No. 5853991
; GENERAL INFORMATION:
; APPLICANT: WANG, Xun
; APPLICANT: DUVICK, Jonathan P.
; APPLICANT: BRIGGS, Steven P.
; TITLE OF INVENTION: PCR-BASED CDNA SUBTRACTIVE CLONING
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,028
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,767
; FILING DATE: 19-MAY-1997
; APPLICATION NUMBER: US 08/481,687
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/325/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-863-028-23

Query Match 2.1%; Score 19; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 906 aggcaaaaaaaaaaaaaaa 924
||||||||||||||||||||
Db 7 AGGCAAAAAAAAAAAAAAA 25

RESULT 13
US-09-248-335-29

```
; Sequence 29, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
;  APPLICANT: MCGONIGLE, BRIAN
;  APPLICANT: O'KEEF, DANIEL
;  TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
;  FILE REFERENCE: CL-1128-A
;  CURRENT APPLICATION NUMBER: US/09/248,335
;  CURRENT FILING DATE: 1999-02-10
;  EARLIER APPLICATION NUMBER: 08/924,759
;  EARLIER FILING DATE: 1997-September-05
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 29
;   LENGTH: 1134
;   TYPE: DNA
;   ORGANISM: maize
US-09-248-335-29


  Query Match             2.1%;  Score 19;  DB 3;  Length 1134;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
           |||||||||||||||||||
Db    1039 aggcaaaaaaaaaaaaaaa 1057


RESULT  14
US-08-672-850-5
; Sequence 5, Application US/08672850
; Patent No. 6140117
;  GENERAL INFORMATION:
;    APPLICANT:  Milbrandt, Jeffrey
;    APPLICANT:  Araki, Toshiyuki
;    TITLE OF INVENTION:  NINJURIN
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/672,850
;      FILING DATE:  24-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Silva, Robin M.
;      REGISTRATION NUMBER:  38,304
;      REFERENCE/DOCKET NUMBER:  A-63610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1235 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-672-850-5


  Query Match             2.1%;  Score 19;  DB 3;  Length 1235;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
           |||||||||||||||||||
Db    1216 AGGCAAAAAAAAAAAAAAA 1234


RESULT  15
US-08-514-014-1
; Sequence 1, Application US/08514014
; Patent No. 5707829
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  Kelleher, Kerry
;    APPLICANT:  Carlin, McKeough
;    TITLE OF INVENTION:  DNA SEQUENCES AND SECRETED PROTEINS
;    TITLE OF INVENTION:  ENCODED THEREBY
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc. -- Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/514,014
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2209 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  38..1447
US-08-514-014-1


  Query Match             2.1%;  Score 19;  DB 1;  Length 2209;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
           |||||||||||||||||||
Db    2162 AGGCAAAAAAAAAAAAAAA 2180


RESULT  16
US-08-833-823-1
; Sequence 1, Application US/08833823
; Patent No. 5969093
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  Kelleher, Kerry
```

```
;    APPLICANT:  Carlin, McKeough
;    TITLE OF INVENTION:  DNA SEQUENCES AND SECRETED PROTEINS
;    TITLE OF INVENTION:  ENCODED THEREBY
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc. -- Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,823
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/514,014
;      FILING DATE:  11-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2209 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  38..1447
US-08-833-823-1


  Query Match             2.1%;  Score 19;  DB 2;  Length 2209;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
           |||||||||||||||||||
Db    2162 AGGCAAAAAAAAAAAAAAA 2180


RESULT  17
US-08-813-150-1
; Sequence 1, Application US/08813150
; Patent No. 6069229
;  GENERAL INFORMATION:
;    APPLICANT:  Mueller, Christopher
;    APPLICANT:  Lebecque, Serge J.E.
;    APPLICANT:  Liu, Yong-Jun
;    APPLICANT:  Dowling, Lynette M.
;    APPLICANT:  Huffine, Constance M.
;    APPLICANT:  Gorman, Daniel M.
;    TITLE OF INVENTION:  MAMMALIAN PROTEINASES; OXIDOREDUCTASES;
;    TITLE OF INVENTION:  RELATED REAGENTS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/813,150
;      FILING DATE:  07-MAR-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  SF0693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-852-9196
;      TELEFAX:  650-496-1200
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  61..1470
US-08-813-150-1


  Query Match             2.1%;  Score 19;  DB 3;  Length 2280;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     906 aggcaaaaaaaaaaaaaaa 924
           |||||||||||||||||||
Db    2184 AGGCAAAAAAAAAAAAAAA 2202


RESULT  18
PCT-US95-09261-1
; Sequence 1, Application PC/TUS9509261
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:  NAME:  BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM
;    APPLICANT:  STREET:  201 West 7th Street
;    APPLICANT:  CITY:  Austin
;    APPLICANT:  STATE:  Texas
;    APPLICANT:  COUNTRY:  United States of America
;    APPLICANT:  POSTAL CODE:  78701
;    APPLICANT:  TELEPHONE NO: (512)499-4462
;    APPLICANT:  TELEFAX:  (512)499-4523
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR THE EXPRESSION OF
;    TITLE OF INVENTION:  A BONE AND PROSTATE DERIVED GROWTH FACTOR
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS/ASCII
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09261
;      FILING DATE:  CONCURRENTLY HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,701
```

```
;       FILING DATE:  01-AUG-1994
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SERTICH, GARY J.
;       REGISTRATION NUMBER:  34,430
;       REFERENCE/DOCKET NUMBER:  UTFC422P--
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (713) 789-2679
;       TELEX:  79-0924
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3171 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "DNA"
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  694..2310
PCT-US95-09261-1


  Query Match             2.1%;  Score 19;  DB 5;  Length 3171;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    905 aaggcaaaaaaaaaaaaaa 923
          |||||||||||||||||||
Db   3153 AAGGCAAAAAAAAAAAAAA 3171


RESULT  19
US-08-612-521-3/c
; Sequence 3, Application US/08612521
; Patent No. 5786463
;  GENERAL INFORMATION:
;    APPLICANT:  Peery, Robert B
;    APPLICANT:  Skatrud, Paul L
;    APPLICANT:  Thornewell, Susan J
;    TITLE OF INVENTION:  MULTIPLE DRUG RESISTANCE GENE OF
;    TITLE OF INVENTION:  CRYPTOCOCCUS NEOFORMANS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Division/AEH
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,521
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamilton, Amy E
;      REGISTRATION NUMBER:  33,894
;      REFERENCE/DOCKET NUMBER:  X-9693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3169
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6143 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  541..1072
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1130..1395
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1443..1872
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1925..2426
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2479..2863
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2913..3009
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  3076..3379
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  3438..3561
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  3614..3776
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  3831..3966
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  4016..4244
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  4291..4438
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  4487..4743
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  4793..4958
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  5006..5113
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  5162..5500
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  5553..5588
US-08-612-521-3


  Query Match             2.1%;  Score 19;  DB 1;  Length 6143;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    905 aaggcaaaaaaaaaaaaaa 923
          |||||||||||||||||||
Db   3036 AAGGCAAAAAAAAAAAAAA 3018


RESULT  20
US-09-091-332A-50
; Sequence 50, Application US/09091332A
; Patent No. 6284462
;  GENERAL INFORMATION:
;    APPLICANT:  SATO, YOSHIHIRO
;    APPLICANT:  TSUJI, AKIHIKO
;    APPLICANT:  SUGA, TAKAYUGI
;    TITLE OF INVENTION:  PROBES AND METHODS FOR POLYNUCLEOTIDE DETECTION
;    NUMBER OF SEQUENCES:  58
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LEYDIG, VOIT & MAYER, LTD.
;      STREET:  TWO PRUDENTIAL PLAZA, SUITE 4900
;      CITY:  CHICAGO
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/091,332A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 97JP3438
;      FILING DATE:  26-SEP-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 96256833
;      FILING DATE:  27-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KILYK JR., JOHN
;      REGISTRATION NUMBER:  30763
;      REFERENCE/DOCKET NUMBER:  72917
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-091-332A-50


  Query Match             1.9%;  Score 18;  DB 4;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db      18 GGCAAAAAAAAAAAAAAA 35


RESULT  21
US-08-120-827-85
; Sequence 85, Application US/08120827
; Patent No. 5525495
;  GENERAL INFORMATION:
;    APPLICANT:  KEENE, JACK D.
;    APPLICANT:  KING, PETER H.
;    APPLICANT:  LEVINE, TODD
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL IN THE
;    TITLE OF INVENTION:  RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
;    TITLE OF INVENTION:  INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/120,827
;      FILING DATE:  15-SEP-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5525495man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  714-158-0 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)413-3000
;      TELEFAX:  (703)413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  85:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  57 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-120-827-85


  Query Match             1.9%;  Score 18;  DB 1;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db      36 GGCAAAAAAAAAAAAAAA 53


RESULT  22
US-08-478-675-85
; Sequence 85, Application US/08478675
; Patent No. 5773246
;  GENERAL INFORMATION:
;    APPLICANT:  KEENE, JACK D.
;    APPLICANT:  KING, PETER H.
;    APPLICANT:  LEVINE, TODD
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL IN THE
;    TITLE OF INVENTION:  RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
;    TITLE OF INVENTION:  INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,675
;      FILING DATE:  07-JUN-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/120,827
;      FILING DATE:  15-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5773246man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  714-158-0 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)413-3000
```

```
;      TELEFAX:  (703)413-2220
;      TELEX:  248855 OPAT UR
;    INFORMATION FOR SEQ ID NO:  85:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH:  57 base pairs
;        TYPE:  nucleic acid
;        STRANDEDNESS:  unknown
;        TOPOLOGY:  unknown
;      MOLECULE TYPE:  cDNA
US-08-478-675-85


  Query Match             1.9%;  Score 18;  DB 1;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db      36 GGCAAAAAAAAAAAAAAA 53


RESULT  23
US-08-721-488-4
; Sequence 4, Application US/08721488
; Patent No. 5965388
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaVallie, Edward
;    APPLICANT:  Racie, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    APPLICANT:  Bowman, Michael
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/721,488
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  308 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-721-488-4


  Query Match             1.9%;  Score 18;  DB 2;  Length 308;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     266 GGCAAAAAAAAAAAAAAA 283


RESULT  24
US-08-943-731-157
 Sequence 157, Application US/08943731
 Patent No. 6265157
  GENERAL INFORMATION:
    APPLICANT:  PROCKOP, DARWIN J.
    APPLICANT:  SPOTILA, LORETTA D.
    APPLICANT:  DELIAS, CONSTANTINOS D.
    APPLICANT:  SEREDA, LARISA
    APPLICANT:  LARSON, ANDREA W.
    APPLICANT:  PACK, MICHAEL
    APPLICANT:  COLIGE, ALAIN
    APPLICANT:  EARLY, JAMES
    APPLICANT:  KORKKO, JARMO
    APPLICANT:  ALA-KOKKO, LEENA, et al.
    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR DETECTING
    TITLE OF INVENTION:  ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
    NUMBER OF SEQUENCES:  666
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
      STREET:  ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
      STREET:  FLR.
      CITY:  PHILADELPHIA
      STATE:  PA
      COUNTRY:  USA
      ZIP:  19103-7086
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/943,731
      FILING DATE:  03-OCT-1997
      CLASSIFICATION:  435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  US 08/212,322
      FILING DATE:  14-MAR-1994
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  US 07/803,628
      FILING DATE:  03-DEC-1991
    ATTORNEY/AGENT INFORMATION:
      NAME:  DOYLE LEARY Ph.D., KATHRYN
      REGISTRATION NUMBER:  36,317
      REFERENCE/DOCKET NUMBER:  9596-27
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  215-965-1284
      TELEFAX:  215-567-2991
      TELEX:  831-494
  INFORMATION FOR SEQ ID NO:  157:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  343 base pairs
      TYPE:  nucleic acid
      STRANDEDNESS:  double
      TOPOLOGY:  linear
    MOLECULE TYPE:  DNA (genomic)
US-08-943-731-157


  Query Match             1.9%;  Score 18;  DB 4;  Length 343;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     226 GGCAAAAAAAAAAAAAAA 243
```

```
RESULT 25
US-09-342-653-1
; Sequence 1, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Rafalski, Antoni
;  TITLE OF INVENTION: Chromatin Associated Proteins
;  FILE REFERENCE: BB-1118
;  CURRENT APPLICATION NUMBER: US/09/342,653
;  CURRENT FILING DATE: 1999-06-29
;  EARLIER APPLICATION NUMBER: 60/092,841
;  EARLIER FILING DATE: July 14, 1998
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
;   LENGTH: 413
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-342-653-1


  Query Match             1.9%;  Score 18;  DB 4;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     387 ggcaaaaaaaaaaaaaaa 404


RESULT 26
US-08-686-878A-13
; Sequence 13, Application US/08686878A
; Patent No. 5708157
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaVallie, Edward
;    APPLICANT:  Racie, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Evans, Cheryl
;    APPLICANT:  Spaulding, Vikki
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/686,878A
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  429 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-686-878A-13


  Query Match             1.9%;  Score 18;  DB 1;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     412 GGCAAAAAAAAAAAAAAA 429


RESULT 27
US-08-702-080-1/c
; Sequence 1, Application US/08702080
; Patent No. 5654173
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaVallie, Edward
;    APPLICANT:  Racie, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/702,080
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-702-080-1


  Query Match             1.9%;  Score 18;  DB 1;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     312 GGCAAAAAAAAAAAAAAA 295


RESULT 28
US-08-858-830-1/c
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; Sequence 1, Application US/08858830
; Patent No. 5965693
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaVallie, Edward
;    APPLICANT:  Racie, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,830
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/702,080
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-858-830-1


  Query Match             1.9%;  Score 18;  DB 2;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     312 GGCAAAAAAAAAAAAAAA 295


RESULT  29
US-08-858-834-1/c
; Sequence 1, Application US/08858834
; Patent No. 5981222
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaVallie, Edward
;    APPLICANT:  Racie, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,834
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/702,080
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-858-834-1


  Query Match             1.9%;  Score 18;  DB 2;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     312 GGCAAAAAAAAAAAAAAA 295


RESULT  30
US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366
;  GENERAL INFORMATION:
;    APPLICANT:  Ulrich Bogdan
;    APPLICANT:  Reinhard Buttner
;    APPLICANT:  Brigitte Kaluza
;    TITLE OF INVENTION:  MELANOMA-INHIBITING PROTEIN
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 1.44 Mb storage diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/578,649
;      FILING DATE:  29-July-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 43 24 247.2
;      FILING DATE:  20-July-1993
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Andrew L. Tiajoloff
;       REGISTRATION NUMBER:  31,575
;       REFERENCE/DOCKET NUMBER:  BOER 1035-PFF/ALT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 688-9200
;       TELEFAX:  (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  581 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  110..499
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  110..178
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  179..499
US-08-578-649-4


  Query Match             1.9%;  Score 18;  DB 1;  Length 581;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db     563 GGCAAAAAAAAAAAAAAA 580


RESULT  31
US-09-385-982-98/c
; Sequence 98, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
;  APPLICANT: ENDEGE, WILSON O., ET AL.
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS:  II
;  FILE REFERENCE: CCDNA-260XX
;  CURRENT APPLICATION NUMBER: US/09/385,982
;  CURRENT FILING DATE: 1999-08-30
;  EARLIER APPLICATION NUMBER: 09/328,111
;  EARLIER FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: 60/117,393
;  EARLIER FILING DATE: 1999-01-27
;  EARLIER APPLICATION NUMBER: 60/098,639
;  EARLIER FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 544
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 98
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(582)
;   OTHER INFORMATION: n = A,T,C or G
US-09-385-982-98


  Query Match             1.9%;  Score 18;  DB 4;  Length 582;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     270 gcctcagtttccttgtct 287
           ||||||||||||||||||
Db     309 GCCTCAGTTTCCTTGTCT 292


RESULT  32
US-09-328-111-572/c
; Sequence 572, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,601
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 572
;   LENGTH: 621
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(621)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-572


  Query Match             1.9%;  Score 18;  DB 4;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db      40 GGCAAAAAAAAAAAAAAA 23


RESULT  33
US-09-461-474-13
; Sequence 13, Application US/09461474
; Patent No. 6278042
; GENERAL INFORMATION:
;  APPLICANT: Allen, Steve
;  APPLICANT: Rafalski, Antoni
;  APPLICANT: Sakai, Hajime
;  TITLE OF INVENTION: Plant Metal Transporters
;  FILE REFERENCE: BB1303 US NA
;  CURRENT APPLICATION NUMBER: US/09/461,474
;  CURRENT FILING DATE: 1999-12-14
;  EARLIER APPLICATION NUMBER: 60/112,562
;  EARLIER FILING DATE: 1998-12-16
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
;   LENGTH: 790
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-461-474-13


  Query Match             1.9%;  Score 18;  DB 4;  Length 790;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    907 ggcaaaaaaaaaaaaaa 924
          ||||||||||||||||||
Db    752 ggcaaaaaaaaaaaaaa 769


RESULT 34
US-08-684-672-25
; Sequence 25, Application US/08684672
; Patent No. 5700926
;  GENERAL INFORMATION:
;    APPLICANT:  KERE, Juha
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  de la CHAPELLE, Albert
;    APPLICANT:  SRIVASTAVA, Anand Kumar
;    TITLE OF INVENTION:  MOLECULAR CLONING OF THE ANHIDROTIC
;    TITLE OF INVENTION:  ECTODERMAL DYSPLASIA GENE
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS, L.L.P.
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,672
;      FILING DATE:  22-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/052,997
;      FILING DATE:  27-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  O'Shaughnessy, Brian P.
;      REGISTRATION NUMBER:  32,747
;      REFERENCE/DOCKET NUMBER:  030956-002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  854 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  243..650
US-08-684-672-25


  Query Match             1.9%;  Score 18;  DB 1;  Length 854;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    906 aggcaaaaaaaaaaaaaa 923
          ||||||||||||||||||
Db    837 AGGCAAAAAAAAAAAAAA 854


RESULT 35
US-08-684-672-26
; Sequence 26, Application US/08684672
; Patent No. 5700926
;  GENERAL INFORMATION:
;    APPLICANT:  KERE, Juha
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  de la CHAPELLE, Albert
;    APPLICANT:  SRIVASTAVA, Anand Kumar
;    TITLE OF INVENTION:  MOLECULAR CLONING OF THE ANHIDROTIC
;    TITLE OF INVENTION:  ECTODERMAL DYSPLASIA GENE
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS, L.L.P.
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,672
;      FILING DATE:  22-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/052,997
;      FILING DATE:  27-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  O'Shaughnessy, Brian P.
;      REGISTRATION NUMBER:  32,747
;      REFERENCE/DOCKET NUMBER:  030956-002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  854 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-684-672-26


  Query Match             1.9%;  Score 18;  DB 1;  Length 854;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    906 aggcaaaaaaaaaaaaaa 923
          ||||||||||||||||||
Db    837 AGGCAAAAAAAAAAAAAA 854


RESULT 36
US-08-896-410-37
; Sequence 37, Application US/08896410
; Patent No. 5834310
;  GENERAL INFORMATION:
;    APPLICANT:  The Government of the United States of America,
;    APPLICANT:  as represented by the Secretary, Department of Health and Human
;    APPLICANT:  Services
;    TITLE OF INVENTION:  Mammalian Muscle NAD:Arginine
;    TITLE OF INVENTION:  ADP-ribosyltransferase
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive, 16th floor
;      CITY:  Newport
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/896,410
;       FILING DATE:  18-JUL-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/454,556
;       FILING DATE:  May 30, 1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Anita M. Kirkpatrick
;       REGISTRATION NUMBER:  32,617
;       REFERENCE/DOCKET NUMBER:  NIH039.001DV1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-235-8550
;       TELEFAX:  619-235-0176
;   INFORMATION FOR SEQ ID NO:  37:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1305 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  73..1047
US-08-896-410-37


  Query Match             1.9%;  Score 18;  DB 2;  Length 1305;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    907 ggcaaaaaaaaaaaaaaa 924
          ||||||||||||||||||
Db   1280 GGCAAAAAAAAAAAAAAA 1297


RESULT  37
US-09-073-297-1
; Sequence 1, Application US/09073297
; Patent No. 6255114
;  GENERAL INFORMATION:
;     APPLICANT:  LIGHTNER, JONATHAN EDWARD
;     TITLE OF INVENTION:  STARCH BIOSYNTHETIC ENZYMES
;     NUMBER OF SEQUENCES:  26
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  E. I. DU PONT DE NEMOURS AND COMPANY
;       STREET:  1007 MARKET STREET
;       CITY:  WILMINGTON
;       STATE:  DELAWARE
;       COUNTRY:  U.S.A.
;       ZIP:  19898
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.50 INCH
;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  MICROSOFT WINDOWS 95
;       SOFTWARE:  MICROSOFT WORD VERSION 7.0A
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/073,297
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/852615
;       FILING DATE:  MAY 7, 1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MAJARIAN, WILLIAM R.
;       REGISTRATION NUMBER:  41,173
;       REFERENCE/DOCKET NUMBER:  BB-1083-B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  302-992-4926
;       TELEFAX:  302-773-0164
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1333 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  2..1039
US-09-073-297-1


  Query Match             1.9%;  Score 18;  DB 4;  Length 1333;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    907 ggcaaaaaaaaaaaaaaa 924
          ||||||||||||||||||
Db   1313 GGCAAAAAAAAAAAAAAA 1330


RESULT  38
US-08-631-200-14
; Sequence 14, Application US/08631200
; Patent No. 5646040
;  GENERAL INFORMATION:
;     APPLICANT:  Kleyn, Patrick W.
;     APPLICANT:  Moore, Karen J.
;     TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;     TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;     NUMBER OF SEQUENCES:  59
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Pennie & Edmonds
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/631,200
;       FILING DATE:  12-APR-1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Coruzzi, Laura A.
;       REGISTRATION NUMBER:  30,742
;       REFERENCE/DOCKET NUMBER:  7853-057
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1338 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..855
US-08-631-200-14


  Query Match             1.9%;  Score 18;  DB 1;  Length 1338;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    907 ggcaaaaaaaaaaaaaaa 924
          ||||||||||||||||||
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Db    1306 GGCAAAAAAAAAAAAAAA 1323


RESULT 39
US-08-829-553-14
; Sequence 14, Application US/08829553
; Patent No. 5817762
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,553
;      FILING DATE:  28-MAR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/631,200
;      FILING DATE:  12-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7853-057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1338 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..855
US-08-829-553-14


  Query Match             1.9%;  Score 18;  DB 1;  Length 1338;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
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Db    1306 GGCAAAAAAAAAAAAAAA 1323


RESULT 40
US-08-922-267A-14
; Sequence 14, Application US/08922267A
; Patent No. 5861239
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  82
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/922,267A
;      FILING DATE:  2-SEP-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/829,553
;      FILING DATE:  28-MAR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/631,200
;      FILING DATE:  12-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7853-085
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1338 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..855
US-08-922-267A-14


  Query Match             1.9%;  Score 18;  DB 2;  Length 1338;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db    1306 GGCAAAAAAAAAAAAAAA 1323


RESULT 41
US-08-936-707A-14
; Sequence 14, Application US/08936707A
; Patent No. 5871931
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/936,707A
;       FILING DATE:  24-SEP-1997
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Coruzzi, Laura A.
;       REGISTRATION NUMBER:  30,742
;       REFERENCE/DOCKET NUMBER:  7853-100
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1338 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..855
US-08-936-707A-14


  Query Match             1.9%;  Score 18;  DB 2;  Length 1338;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
           ||||||||||||||||||
Db    1306 GGCAAAAAAAAAAAAAAA 1323


RESULT  42
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; Sequence 14, Application US/08936706A
; Patent No. 5876919
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/936,706A
;      FILING DATE:  24-SEP-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7853-099
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1338 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..855
US-08-936-706A-14


  Query Match             1.9%;  Score 18;  DB 2;  Length 1338;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     907 ggcaaaaaaaaaaaaaaa 924
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Db    1306 GGCAAAAAAAAAAAAAAA 1323


RESULT  43
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; Sequence 14, Application US/09248203
; Patent No. 6043346
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/248,203
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/936,707
;      FILING DATE:  24-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7853-100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1338 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      NAME/KEY:  CDS
;      LOCATION:  1..855
US-09-248-203-14


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  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db   1306 GGCAAAAAAAAAAAAAAA 1323


RESULT 44
US-09-406-071-14
; Sequence 14, Application US/09406071
; Patent No. 6207386
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;    CURRENT APPLICATION DATA:
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;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/936,707
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7853-100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1338 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..855
US-09-406-071-14


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Qy    907 ggcaaaaaaaaaaaaaaa 924
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Db   1306 GGCAAAAAAAAAAAAAAA 1323


RESULT 45
US-08-955-918C-4
; Sequence 4, Application US/08955918C
; Patent No. 6268130
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick, and Moore, Karen
;    TITLE OF INVENTION:  RP Compositions and Therapeutic and
;    TITLE OF INVENTION:  Diagnostic Uses Therefor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/955,918C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/697,766
;      FILING DATE:  29-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MNI-007CPDV2CPA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1338 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..858
US-08-955-918C-4


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Qy    907 ggcaaaaaaaaaaaaaaa 924
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Db   1306 GGCAAAAAAAAAAAAAAA 1323


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Job time: 10159 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 30, 2002, 11:14:38 ; Search time 728.83 Seconds
(without alignments)
694.019 Million cell updates/sec

Title: US-09-248-178-67
Perfect score: 590
Sequence: 1 gtgctctgtgtatttttta.....tatttaaaaaaaaaaaaaaa 590

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 10

Total number of hits satisfying chosen parameters: 356342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		590	100.0	590	20	AAX84213	DNA encoding human
2		590	100.0	590	21	AAC79442	cDNA sequence of h
c 3		430	72.9	7221	22	AAI57697	Human colorectal c
c 4		427	72.4	629	22	AAI57595	Human colorectal c
c 5		23	3.9	468	22	AAH68826	Human cervical can
c 6		23	3.9	543	22	AAH70254	Human cervical can
7		22	3.7	638	21	AAC96909	Human secreted pro
8		22	3.7	1053	19	AAV34234	Human secreted pro
9		22	3.7	1075	19	AAV34235	Human secreted pro
10		22	3.7	1105	19	AAV34169	Human secreted pro
11		22	3.7	5198	7	AAN60009	Sequence of human
12		22	3.7	34488	22	AAF97854	Human neuroblastom
13		22	3.7	121162	21	AAC66548	Human kinesin-like
14		21	3.6	67	22	AAF50545	Probe #2 used in a
15		21	3.6	679	15	AAQ74410	Lipid transfer pro
16		21	3.6	959	19	AAV59132	Nucleotide sequenc
c 17		21	3.6	1049	21	AAF22420	Human secreted pro
18		21	3.6	1070	20	AAX20486	Human secreted pro
19		21	3.6	1164	21	AAC93427	Human secreted pro
20		21	3.6	1279	21	AAC78079	Human cancer assoc
21		21	3.6	1279	22	AAH34582	Human colon cancer
22		21	3.6	1302	17	AAT17380	DNA encoding endot
23		21	3.6	1302	19	AAV53733	Nucelotide sequenc
24		21	3.6	1302	21	AAA07076	cDNA encoding memb
25		21	3.6	1373	21	AAZ98076	Human secreted pro
26		21	3.6	1373	22	AAD11689	Human secreted pro
27		21	3.6	1547	22	AAC91065	Mouse ortholog of
28		21	3.6	1549	22	AAD08465	Human secreted pro
29		21	3.6	1624	16	AAQ85984	Oryza sativa pPFK-
30		21	3.6	1763	22	AAI58747	Human polynucleoti
31		21	3.6	1994	22	AAH48294	Honeybee alpha-glu
32		21	3.6	2281	20	AAZ33647	Human breast tumou
33		21	3.6	3133	16	AAQ90652	Eph-related tyrosi
34		21	3.6	3831	22	AAH19355	Porcine CD29 prote
c 35		21	3.6	5306	20	AAX35681	Renal cancer assoc
c 36		21	3.6	5760	6	AAN50530	Sequence encoding
37		21	3.6	5830	21	AAC77811	Human cancer assoc
c 38		20	3.4	35	20	AAX76366	Pneumocystis carin
c 39		20	3.4	40	20	AAX76360	Pneumocystis carin
c 40		20	3.4	42	17	AAT17027	Human mitochondria
41		20	3.4	51	21	AAA61354	Model mRNA #3 used
42		20	3.4	79	19	AAV26706	Human novel secret
43		20	3.4	115	21	AAA61347	Model RNA substrat
c 44		20	3.4	242	21	AAA31926	Plant microsatelli
45		20	3.4	278	20	AAZ08301	Human lung tumour

ALIGNMENTS

RESULT 1
AAX84213
ID AAX84213 standard; cDNA; 590 BP.
XX
AC AAX84213;
XX
DT 08-SEP-1999 (first entry)
XX
DE DNA encoding human breast tumour protein immunogenic fragment.
XX
KW Breast tumour protein; immunogenic fragment; vaccine; detection;
KW breast cancer development; therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9933869-A2.
XX
PD 08-JUL-1999.
XX
PF 22-DEC-1998; 98WO-US27416.
XX
PR 17-JUL-1998; 98US-0118627.
PR 24-DEC-1997; 97US-0998253.
PR 24-DEC-1997; 97US-0998255.
PR 17-JUL-1998; 98US-0118554.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J;
XX
DR WPI; 1999-405486/34.
XX
PT New breast tumour protein genes used, in vaccines for immunotherapy,
PI or for diagnosis of breast cancer

```
XX
PS   Claim 3; Page 62; 70pp; English.
XX
CC   This sequence encodes a human breast tumour protein immunogenic fragment
CC   of the invention. The polypeptides or nucleic acids encoding them are
CC   useful in vaccines and pharmaceutical compositions for manufacture of
CC   medicaments for inhibiting the development of breast cancer in a patient.
CC   They can also be used to treat breast cancer. Antibodies against these
CC   polypeptides can be used to detect and monitor progression of breast
CC   cancer in patients. Primers and probes derived from the polynucleotides
CC   encoding the breast proteins are useful for detection of breast cancer.
CC   Peripheral blood cells from a patient incubated in the presence of at
CC   least one polypeptide, such that T cells proliferate, are useful in
CC   manufacture of a medicament for treating breast cancer in a patient.
CC   Antigen presenting cells incubated in the presence of at least one
CC   polypeptide are also useful for treating breast cancer.
XX
SQ   Sequence 590 BP; 197 A; 82 C; 80 G; 231 T; 0 other;


  Query Match             100.0%;  Score 590;  DB 20;  Length 590;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-211;
  Matches  590;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 gtgctctgtgtatttttttactgcattagacattgaatagtaatttgcgttaagatacgc 60

Qy     61 ttaaaggctctttgtgaccatgtttccctttgtagcaataaaatgtttttttacgaaaact 120
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Qy    121 ttctccctggattagcagtttaaatgaaacagagttcatcaatgaaatgagtatttaaaa 180
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Qy    181 taaaaatttgccttaatgtatcagttcagctcacaagtattttaagatgattgagaagac 240
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Db    181 taaaaatttgccttaatgtatcagttcagctcacaagtattttaagatgattgagaagac 240

Qy    241 ttgaattaaagaaaaaaaaaattctcaatcatatttttaaaatataagactaaaattgttt 300
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Db    241 ttgaattaaagaaaaaaaaaattctcaatcatatttttaaaatataagactaaaattgttt 300

Qy    301 ttaaaacacatttcaaatagaagtgagtttgaactgaccttatttatactctttttaagt 360
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Db    301 ttaaaacacatttcaaatagaagtgagtttgaactgaccttatttatactctttttaagt 360

Qy    361 ttgttcctttttcccctgtgcctgtgtcaaatcttcaagtcttgctgaaaatacatttgata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ttgttcctttttcccctgtgcctgtgtcaaatcttcaagtcttgctgaaaatacatttgata 420

Qy    421 caaagttttctgtagttgtgttagttcttttgtcatgtctgttttggctgaagaaccaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    481 gaagcagactttttctttaaaagaattatttctctttcaaatatttctatcttttttaaa 540
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Db    481 gaagcagactttttctttaaaagaattatttctctttcaaatatttctatcttttttaaa 540

Qy    541 aaattccttttatggcttatatacctacatatttaaaaaaaaaaaaaa 590
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Db    541 aaattccttttatggcttatatacctacatatttaaaaaaaaaaaaaa 590


RESULT   2
AAC79442
ID   AAC79442 standard; cDNA; 590 BP.
XX
AC   AAC79442;
XX
DT   07-FEB-2001  (first entry)
XX
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DE   DNA sequence of human breast tumour clone lu15B2.
XX
KW   Cancer; breast tumour antigen; cytostatic; immunotherapy;
KW   breast cancer; vaccine; SS.
XX
OS   Homo sapiens.
XX
PN   WO200061756-A2.
XX
PD   19-OCT-2000.
XX
PF   07-APR-2000; 2000WO-US09688.
XX
PR   09-APR-1999;   99US-0288950.
PR   12-JUL-1999;   99US-0346327.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Reed SG, Xu J, Dillon DC;
XX
DR   WPI; 2000-636516/61.
XX
PT   Novel isolated polypeptide comprising an immunogenic portion of a
PT   breast cancer protein useful in the detection and treatment of breast
PT   cancer -
XX
PS   Claim 4; Page 79; 95pp; English.
XX
CC   The present sequence was isolated from a breast tumour cDNA library. It
CC   is provided in a specification relating to compounds for immunotherapy
CC   and diagnosis of breast cancer. Breast tumour antigens and the
CC   polynucleotides that encode them may be used in the production of a
CC   pharmaceutical composition to be used in the treatment of breast cancer.
CC   Proliferated T cells and incubated antigen presenting cells are also
CC   required. The polypeptides and polynucleotides may also be used to
CC   produce a vaccine.
XX
SQ   Sequence 590 BP; 197 A; 82 C; 80 G; 231 T; 0 other;


  Query Match             100.0%;  Score 590;  DB 21;  Length 590;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-211;
  Matches  590;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgctctgtgtatttttttactgcattagacattgaatagtaatttgcgttaagatacgc 60
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Qy    241 ttgaattaaagaaaaaaaaaattctcaatcatatttttaaaatataagactaaaattgttt 300
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Qy    301 ttaaaacacatttcaaatagaagtgagtttgaactgaccttatttatactctttttaagt 360
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RESULT   3
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ID   AAI57697 standard; DNA; 7221 BP.
XX
AC   AAI57697;
XX
DT   19-OCT-2001  (first entry)
XX
DE   Human colorectal cancer antigen coding sequence SEQ ID NO: 234.
XX
KW   Human; colorectal cancer; colorectal cancer antigen; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155350-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01350.
XX
PR   31-JAN-2000; 2000US-0179065.
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PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Barash SC, Ruben SM;
XX
DR   WPI; 2001-457727/49.
XX
PT   Isolated polypeptide for treating, preventing and/ or prognosing
PT   disorders related to the colon and rectum including colorectal cancers
PT   and also for testing and detection e.g. diagnosis -
XX
PS   Disclosure; SEQ ID NO: 234; 522pp + Sequence Listing; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of colorectal cancer antigens. These are shown in
CC   AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the
CC   diagnosis, prevention and treatment of cancer of the colon and/or rectum.
CC   The present sequence is a colorectal cancer antigen genomic sequence.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 7221 BP; 2552 A; 1315 C; 1263 G; 2091 T; 0 other;


  Query Match           72.9%;  Score 430;  DB 22;  Length 7221;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-152;
  Matches  430;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgctctgtgtatttttttactgcattagacattgaatagtaatttgcgttaagatacgc 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 GTGCTCTGTGTATTTTTTTACTGCATTAGACATTGAATAGTAATTTGCGTTAAGATACGC 371

Qy     61 ttaaaggctctttgtgaccatgtttccctttgtagcaataaaatgttttttacgaaaact 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 TTAAAGGCTCTTTGTGACCATGTTTCCCTTTGTAGCAATAAAATGTTTTTTACGAAAACT 311

Qy    121 ttctccctggattagcagtttaaatgaaacagagttcatcaatgaaatgagtatttaaaa 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TTCTCCCTGGATTAGCAGTTTAAATGAAACAGAGTTCATCAATGAAATGAGTATTTAAAA 251

Qy    181 taaaaatttgccttaatgtatcagttcagctcacaagtattttaagatgattgagaagac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 TAAAAATTTGCCTTAATGTATCAGTTCAGCTCACAAGTATTTTAAGATGATTGAGAAGAC 191

Qy    241 ttgaattaaagaaaaaaaaattctcaatcatatttttaaaatataagactaaaattgttt 300
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Db    190 TTGAATTAAAGAAAAAAAAATTCTCAATCATATTTTTAAAATATAAGACTAAAATTGTTT 131

Qy    301 ttaaaacacatttcaaatagaagtgagtttgaactgaccttatttatactctttttaagt 360
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Db    130 TTAAAACACATTTCAAATAGAAGTGAGTTTGAACTGACCTTATTTATACTCTTTTTAAGT 71

Qy    361 ttgttccttttccctgtgcctgtgtcaaatcttcaagtcttgctgaaaatacatttgata 420
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Db     70 TTGTTCCTTTTCCCTGTGCCTGTGTCAAATCTTCAAGTCTTGCTGAAAATACATTTGATA 11

Qy    421 caaagttttc 430
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Db     10 CAAAGTTTTC 1


RESULT   4
AAI57595/c
ID   AAI57595 standard; cDNA; 629 BP.
XX
AC   AAI57595;
XX
DT   19-OCT-2001  (first entry)
XX
DE   Human colorectal cancer antigen cDNA SEQ ID NO: 59.
XX
KW   Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155350-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01350.
XX
PR   31-JAN-2000; 2000US-0179065.
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PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-457727/49.
DR P-PSDB; AAM38617.
XX
PT Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the colon and rectum including colorectal cancers
PT and also for testing and detection e.g. diagnosis -
XX
PS Claim 1; SEQ ID NO: 59; 522pp - Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of colorectal cancer antigens. These are shown in
CC AA157547-AA157619 and AAM38569-AAM38641. These can be used in the
CC diagnosis, prevention and treatment of cancer of the colon and/or rectum.
CC The present sequence is a colorectal cancer antigen coding sequence of
CC the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 629 BP; 244 A; 94 C; 79 G; 212 T; 0 other;

Query Match 72.4%; Score 427; DB 22; Length 629;
Best Local Similarity 100.0%; Pred. No: 1.6e-150;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 gtgctctgtgtatttttttactgcattagacattgaatagtaatttgcgttaagatacgc 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 GTGCTCTGTGTATTTTTTTACTGCATTAGACATTGAATAGTAATTTGCGTTAAGATACGC 379

Qy     61 ttaaaggctctttgtgaccatgtttccctttgtagcaataaaatgtttttttacgaaaact 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 TTAAAGGCTCTTTGTGACCATGTTTCCCTTTGTAGCAATAAAATGTTTTTTACGAAAACT 319

Qy    121 ttctccctggattagcagtttaaatgaaacagagttcatcaatgaaatgagtatttaaaa 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 TTCTCCCTGGATTAGCAGTTTAAATGAAACAGAGTTCATCAATGAAATGAGTATTTAAAA 259

Qy    181 taaaaatttgccttaatgtatcagttcagctcacaagtatttttaagatgattgagaagac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 TAAAAATTTGCCTTAATGTATCAGTTCAGCTCACAAGTATTTTTAAGATGATTGAGAAGAC 199

Qy    241 ttgaattaaagaaaaaaaaaattctcaatcatatttttaaaatataagactaaaattgttt 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 TTGAATTAAAGAAAAAAAAAATTCTCAATCATATTTTTAAAATATAAGACTAAAATTGTTT 139

Qy    301 ttaaaacacatttcaaatagaagtgagtttgaactgaccttatttatactctttttaagt 360
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 TTAAAACACATTTCAAATAGAAGTGAGTTTGAACTGACCTTATTTATACTCTTTTTAAGT 79

Qy    361 ttgttcctttcccctgtgcctgtgtcaaatcttcaagtcttgctgaaaatacatttgata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 TTGTTCCTTTTCCCTGTGCCTGTGTCAAATCTTCAAGTCTTGCTGAAAATACATTTGATA 19

Qy    421 caaagtt 427
          |||||||
Db     18 CAAAGTT 12


RESULT   5
AAH68826/c
ID   AAH68826 standard; cDNA; 468 BP.
XX
AC   AAH68826;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human cervical cancer marker nucleic acid 100.
XX
KW   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142467-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33312.
XX
PR   08-DEC-1999;   99US-0169681.
PR   21-DEC-1999;   99US-0171350.
PR   14-MAR-2000; 2000US-0189315.
PR   12-MAY-2000; 2000US-0203791.
PR   09-JUN-2000; 2000US-0210600.
PR   21-JUL-2000; 2000US-0220114.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Deeds J,  Berger A,  Zhao X;
XX
DR   WPI; 2001-375006/39.
XX
PT   New isolated nucleic acid for diagnosing and treating cervical cancer
PT   and for assessing and detecting compounds for treating the cancer -
XX
PS   Claim 1; Page 120-121; 1051pp; English.
XX
CC   The invention relates to novel genes (AAH68727-AAH73383) associated with
CC   cervical cancer with cytostatic activity. The nucleic acids and encoded
CC   polypeptides are useful: to assess if a patient is afflicted with
CC   cervical cancer or has a pre-malignant condition; to monitor the
CC   progression of cervical cancer or a premalignant condition in a patient;
CC   and to select and/or assess the efficacy of a compound or therapy for
CC   inhibiting cervical cancer in a patient. The nucleic acids may also be
CC   useful for gene therapy.
XX
SQ   Sequence 468 BP; 121 A; 80 C; 95 G; 168 T; 4 other;


  Query Match             3.9%;  Score 23;  DB 22;  Length 468;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    568 acatatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||||
Db     66 ACATATTTAAAAAAAAAAAAAA 44


RESULT   6
AAH70254/c
ID   AAH70254 standard; cDNA; 543 BP.
XX
AC   AAH70254;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human cervical cancer marker nucleic acid 1526.
XX
KW   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142467-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33312.
XX
PR   08-DEC-1999;   99US-0169681.
PR   21-DEC-1999;   99US-0171350.
PR   14-MAR-2000; 2000US-0189315.
PR   12-MAY-2000; 2000US-0203791.
PR   09-JUN-2000; 2000US-0210600.
PR   21-JUL-2000; 2000US-0220114.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Deeds J,  Berger A,  Zhao X;
XX
DR   WPI; 2001-375006/39.
XX
PT   New isolated nucleic acid for diagnosing and treating cervical cancer
PT   and for assessing and detecting compounds for treating the cancer -
XX
PS   Claim 1; Page 343; 1051pp; English.
XX
CC   The invention relates to novel genes (AAH68727-AAH73383) associated with
CC   cervical cancer with cytostatic activity. The nucleic acids and encoded
CC   polypeptides are useful: to assess if a patient is afflicted with
CC   cervical cancer or has a pre-malignant condition; to monitor the
CC   progression of cervical cancer or a premalignant condition in a patient;
CC   and to select and/or assess the efficacy of a compound or therapy for
CC   inhibiting cervical cancer in a patient. The nucleic acids may also be
CC   useful for gene therapy.
XX
SQ   Sequence 543 BP; 134 A; 103 C; 117 G; 189 T; 0 other;


  Query Match             3.9%;  Score 23;  DB 22;  Length 543;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    568 acatatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||||
Db     77 ACATATTTAAAAAAAAAAAAAA 55


RESULT   7
AAC96909
ID   AAC96909 standard; cDNA; 638 BP.
XX
AC   AAC96909;
XX
DT   22-FEB-2001  (first entry)
XX
DE   Human secreted protein cDNA #10.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein; ss.
XX
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OS Homo sapiens.
XX
PN WO200061624-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US08980.
XX
PR 09-APR-1999; 99US-0128700.
PR 20-JAN-2000; 2000US-0176930.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-656324/63.
DR P-PSDB; AAB52112.
XX
PT New nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX
PS Claim 1; Page 400; 478pp; English.
XX
CC The invention relates to the isolation of genes AAC96900-C96947 encoding
CC 48 human secreted proteins AAB52104-B52150. The genes can be used to
CC generate fusion proteins by linking to the gene for the human
CC immunoglobulin G Fc portion (SEQIDI) for increasing the stability of
CC the fusion protein as compared to the human protein only. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated
CC from a range of human tissues disclosed in the specification. The
CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
SQ Sequence 638 BP; 174 A; 148 C; 147 G; 169 T; 0 other;

Query Match 3.7%; Score 22; DB 21; Length 638;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 569 catatttaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 599 catatttaaaaaaaaaaaaaa 620

RESULT 8
AAV34234
ID AAV34234 standard; DNA; 1053 BP.
XX
AC AAV34234;
XX
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein gene 16 clone HMABH07.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04492.
XX
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043315.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 05-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.

PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Graves KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
DR WPI; 1998-609887/51.
DR P-PSDB; AAW75137.
XX
PT New isolated human genes and the secreted polypeptides they encode
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 234; 447pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34145) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).
XX
SQ Sequence 1053 BP; 248 A; 298 C; 295 G; 209 T; 3 other;

Query Match 3.7%; Score 22; DB 19; Length 1053;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 569 catatttaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 1014 catatttaaaaaaaaaaaaaa 1035

RESULT 9
AAV34235
ID AAV34235 standard; DNA; 1075 BP.
XX
AC AAV34235;
XX
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein gene.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04492.
XX
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
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PR 07-MAR-1997; 97US-0040626.
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PR 11-APR-1997; 97US-0043578.
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PR 23-MAY-1997; 97US-0047601.
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PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
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PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057761.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Graves RA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
DR WPI; 1998-609887/51.
DR P-PSDB; AAW75138.
XX
PT New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 234-235; 447pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobuli
CC Fc portion (e.g. AAW34145) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAW34154-W34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAW34154 for described uses).
XX
SQ Sequence 1075 BP; 251 A; 308 C; 302 G; 212 T; 2 other;

Query Match 3.7%; Score 22; DB 19; Length 1075;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 569 catatttaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 1030 catatttaaaaaaaaaaaaaa 1051

RESULT 10
AAW34169
ID AAW34169 standard; DNA; 1105 BP.
XX
AC AAW34169;
XX
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein gene 16 clone HMABH07.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04492.
XX
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043315.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.

PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057751.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Graves KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Puben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
DR WPI; 1998-609887/51.
DR P-PSDB; AAW75072.
XX
PT New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 176; 447pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34145) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences; AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).
XX
SQ Sequence 1105 BP; 259 A; 314 C; 296 G; 226 T; 10 other;

Query Match 3.7%; Score 22; DB 19; Length 1105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 569 catatttaaaaaaaaaaaaaa 590
|||||||||||||||||||||
Db 1034 catatttaaaaaaaaaaaaaa 1055

RESULT 11
AAN60009
ID AAN60009 standard; cDNA; 5198 BP.
XX
AC AAN60009;
XX
DT 30-JUL-1991 (first entry)
XX
DE Sequence of human insulin receptor (hIR) precursor cDNA.
XX
KW Therapy; diagnosis; insulin; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 49..120
FT /*tag= a
FT CDS 121..2289
FT /*tag= b
FT /product= alpha subunit
FT CDS 2290..4150
FT /*tag= c
FT /product= beta subunit
FT misc_feature 2278..2289
FT /*tag= d
FT /note= "precursor processing site"
FT polyA_signal 5160..5165
FT /*tag= e
XX
PN EP192392-A.
XX
PD 27-AUG-1986.
XX

PF 10-FEB-1986; 86EP-0300894.
XX
PR 12-FEB-1985; 85US-0700776.
XX
PA (GETH) GENENTECH INC.
XX
PI Bell JR, Ulrich A, Ramachandran J;
XX
DR WPI; 1986-226966/35.
DR P-PSDB; AAP60005.
XX
PT New DNA encoding insulin receptor or its fragments - used for
PT synthesis of receptor and mutants for therapeutic and diagnostic
PT use
XX
PS Disclosure; Fig 1B; 62pp; English.
XX
CC A mutant IR is claimed which may have a mutated alpha-chain, esp. at
CC the precursor processing site. The beta-chain may be mutated, e.g.
CC by deletion of the transmembrane sequence; the tyrosine kinase
CC activity may be inactivated. Fig. 5 is a comparison of oncogene and
CC human EGF receptor sequences with that of HIR in the cytoplasmic
CC domain of the insulin receptor beta subunit.
XX
SQ Sequence 5198 BP; 1237 A; 1363 C; 1390 G; 1208 T; 0 other;

Query Match 3.7%; Score 22; DB 7; Length 5198;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 569 catatttaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 5173 catatttaaaaaaaaaaaaaa 5194

RESULT 12
AAF97854
ID AAF97854 standard; DNA; 34488 BP.
XX
AC AAF97854;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:69.
XX
KW Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer;
KW tumour suppressor; human 1p36 homozygosity deletion domain; tumour;
KW diagnosis; ds.
XX
OS Homo sapiens.
XX
PN WO200116311-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-JP05930.
XX
PR 31-AUG-1999; 99JP-0245962.
PR 09-MAY-2000; 2000JP-0136265.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
PI Nakagawara A;
XX
DR WPI; 2001-226686/23.
XX
PT Human 1p36 homozygosity deletion domain from the 36-position of first
PT chromosome short arm in human neuroblastoma cell lines, applicable e.g.
PT in gene diagnosis of tumors as well as in developing anti-cancer drugs
PT -
XX
PS Example 8; Page 104-118; 226pp; Japanese.
XX
CC The present invention describes a homozygosity deletion domain
CC co-existing in the 36-position of the first chromosome short arm (1p36)
CC in human neuroblastoma. Also described are base sequences from the 1p36
CC position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1),
CC which are tumour suppressor genes in human neuroblastoma. The genes are
CC tumour suppressor genes, base sequence data of which are applicable as
CC tumour markers and reagents in studying mechanism of tumour body
CC formation, and gene diagnosis of tumours as well as in developing
CC anti-cancer drugs. AAF97787 to AAF97829 represent PCR primers used in
CC the exemplification of the present invention, and AAF97830 to AAF97874
CC represent sequences given in the exemplification of the present
CC invention.
XX
SQ Sequence 34488 BP; 9654 A; 6717 C; 6926 G; 11191 T; 0 other;

Query Match 3.7%; Score 22; DB 22; Length 34488;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 569 catatttaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 20758 catatttaaaaaaaaaaaaaa 20779

RESULT 13
AAC66548
ID AAC66548 standard; DNA; 121162 BP.
XX
AC AAC66548;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 1.
XX
KW Human; kinesin-like protein; HKLP; KIF1; cell division; cancer;
KW intracellular transport; neurological disorder; infertility;
KW biallelic marker; spontaneous abortion; neonatal chromosome disorder;
KW aneuploidy; ds.
XX
OS Homo sapiens.
XX
PN WO200053375-A1.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000WO-IB00552.
XX
PR 20-APR-1999; 99US-0130217.
XX
PA (GEST) GENSET.
XX
PI Bougueleret L, Dufaure-Gare I, Grel P;
XX
DR WPI; 2000-665242/64.
XX
PT An isolated or purified human kinesin-like protein (HKLP) encoding
PT polynucleotide used to detect HKLP polynucleotides in a sample
PT comprises a contiguous span of at least 12 nucleotides -
XX
PS Claim 1; Page 143-175; 199pp; English.
XX
CC The present invention describes the coding and protein sequences of the
CC human kinesin-like protein HKLP. It is thought that the protein could be
CC involved in neurological disorders, infertility, spontaneous abortion,
CC neonatal chromosome disorders, aneuploidy and cancers. This is due to its
CC function in the movement of microtubules. The protein shows homology to
CC the murine KIF1A and KIF1B proteins. The sequences disclosed in the
CC invention can be used in the isolation of similar human proteins and in
CC vector production. In addition, the biallelic markers shown can be used
CC in disease diagnosis and population studies.

```
XX
SQ   Sequence 121162 BP; 33272 A; 24108 C; 25842 G; 37919 T; 21 other;


  Query Match             3.7%;  Score 22;  DB 21;  Length 121162;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     569 catatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||||
Db   47604 catatttaaaaaaaaaaaaaa 47625


RESULT  14
AAF60545
ID   AAF60545 standard; DNA; 57 BP.
XX
AC   AAF60545;
XX
DT   27-APR-2001  (first entry)
XX
DE   Probe #2 used in a method for quantifying analyte polynucleotides.
XX
KW   Probe; HIV; ss.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO200107661-A2.
XX
PD   01-FEB-2001.
XX
PF   21-JUL-2000; 2000WO-US20034.
XX
PR   23-JUL-1999;   99US-0145432.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Nunomura K;
XX
DR   WPI; 2001-182804/18.
XX
PT   Detecting and quantitating analyte polynucleotide in a sample, by
PT   co-amplifying analyte polynucleotide with predetermined amount of
PT   pseudo target, producing amplification products and quantifying analyte
PT   amplicons -
XX
PS   Example 3; Page 39; 78pp; English.
XX
CC   The present invention relates to a method for quantifying analyte
CC   polynucleotides (AP). The method comprises combining a test sample of AP
CC   with predetermined amount of a pseudo target (PT) and co-amplifying, to
CC   produce a collection of amplification products including an analyte
CC   amplicon if the sample contained AP and PT amplicon. The analyte amplicon
CC   is quantified without reference to the amount of PT amplicon and related
CC   to AP in the sample. The present sequence is a probe used in the method
CC   of the present invention.
XX
SQ   Sequence 67 BP; 36 A; 9 C; 5 G; 17 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 22;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||||
Db      32 atatttaaaaaaaaaaaaaa 52


RESULT  15
AAQ74410
ID   AAQ74410 standard; DNA; 679 BP.
XX
AC   AAQ74410;
XX
DT   12-JUN-1995  (first entry)
XX
DE   Lipid transfer protein coding sequence.
XX
KW   Lipid transfer protein; membrane; liposome; drug carrier; ss.
XX
OS   Spinacia oleracea L.
XX
PN   JP06247999-A.
XX
PD   06-SEP-1994.
XX
PF   24-FEB-1993;   93JP-0035821.
XX
PR   24-FEB-1993;   93JP-0035821.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 1994-322194/40.
DR   P-PSDB; AAR63755.
XX
PT   New lipid transfer protein and its gene - useful for changing the
PT   composition of lipid membranes
XX
PS   Claim 2; Page 2; 10pp; Japanese.
XX
CC   The lipid transfer protein encoded by this sequence may be used to
CC   alter the composition of lipid membranes.  The lipid transfer
CC   protein may also be used to create new liposomes for use as drug
CC   carriers and new plants which have cells with altered membranes.
XX
SQ   Sequence 679 BP; 167 A; 134 C; 155 G; 223 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 15;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||||
Db     656 atatttaaaaaaaaaaaaaa 676


RESULT  16
AAV59132
ID   AAV59132 standard; DNA; 959 BP.
XX
AC   AAV59132;
XX
DT   07-JAN-1999  (first entry)
XX
DE   Nucleotide sequence of murine HELA2.
XX
KW   Serine protease; regulation; cell activity; viability; HELA2; ATC2;
KW   BCOM3; testisin; fertility; suppressor; testicular germ cell cancer;
KW   seminoma; testis-specific expression; antitumour; sperm development;
KW   infertility; mouse; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             2..859
FT                   /*tag= a
FT                   /product= HELA2
XX
PN   WO9836054-A1.
XX
PD   20-AUG-1998.
XX
PF   13-FEB-1998;   98WO-AU00085.
XX
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FR   18-NOV-1997;   97AU-0000422.
FR   13-FEB-1997;   97AU-0005101.
XX
FA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Antalis TM,  Hooper JD;
XX
DR   WPI; 1998-480768/41.
DR   P-PSDB; AAW77301.
XX
PT   New serine protease(s) and kinase involved in regulating cell
PT   activity and viability - particularly the testis-specific protease
PT   HELA2 used for modulation of fertility and as tumour suppressor
XX
PS   Example 14; Fig 18A; 167pp; English.
XX
CC   The present sequence represents the nucleotide sequence of murine HELA2.
CC   Human HELA2 was isolated from HeLa cells. HELA2 has high homology to
CC   serine proteases. The protein is involved in or associated with
CC   regulation of cell activity and/or viability. Administration of
CC   recombinant HELA2 (also called testisin) is used to increase fertility.
CC   Downregulation of HELA2 reduces fertility. HELA2 is also a suppressor of
CC   testicular germ cell cancers (seminoma) and is also expressed in some
CC   non-testicular cancers (of colon, pancreas, prostate and ovary), so is
CC   a marker/potential therapeutic target for cancer. The promoter from the
CC   HELA2 gene is useful for testis-specific expression of other genes,
CC   e.g. for gene therapy or modulation of fertility. Drugs that block
CC   activity of HELA2 should have antitumour activity (other than in
CC   testis) while in testis recombinant HELA2 should stop growth of tumours
CC   and normalise sperm development (eliminating the need for orchidectomy).
CC   Identification of mutant forms of HELA2 can be used to diagnose
CC   infertility.
XX
SQ   Sequence 959 BP; 225 A; 262 C; 241 G; 231 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 19;  Length 959;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaaa 590
           |||||||||||||||||||||
Db     934 atatttaaaaaaaaaaaaaaa 954


RESULT  17
AAF22420/c
ID   AAF22420 standard; cDNA; 1049 BP.
XX
AC   AAF22420;
XX
DT   26-MAR-2001  (first entry)
XX
DE   Human secreted protein gene 48 SEQ ID NO:58.
XX
KW   Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW   antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW   cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW   fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
KW   rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
KW   cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
KW   angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW   ocular disorder; corneal infection; wound healing; skin aging;
KW   food additive; preservative; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061629-A1.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US09071.
XX
PR   09-APR-1999;   99US-0128694.
PR   20-JAN-2000;  2000US-0176931.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Ruben SM,  Komatsoulis G;
XX
DR   WPI; 2000-647420/62.
DR   P-PSDB; AAB63181.
XX
PT   Isolated nucleic acid molecule encoding a human secreted protein is
PT   used in preventing, treating or ameliorating a medical condition -
XX
PS   Claim 1; Page 458; 533pp; English.
XX
CC   AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
CC   to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
CC   and polypeptides homologous to them. Human secreted proteins have
CC   activities based on the tissues and cells the genes are expressed in.
CC   Examples of activities include: immunosuppressive; antiarthritic;
CC   antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC   cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
CC   fungicide; and ophthalmological. The polynucleotides and proteins can be
CC   used to prevent, treat or ameliorate a medical condition in e.g. humans,
CC   mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
CC   also used in diagnosing a pathological condition or susceptibility to a
CC   pathological condition. Disorders which are diagnosed or treated include
CC   autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC   disorders e.g. neoplasms of the breast or liver, cardiovascular
CC   disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
CC   ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's
CC   disease, infections caused by bacteria, viruses and fungi and ocular
CC   disorders e.g. corneal infection. The polypeptides can also be used to
CC   aid wound healing and epithelial cell proliferation, to prevent skin
CC   aging due to sunburn, to maintain organs before transplantation, for
CC   supporting cell culture of primary tissues, to regenerate tissues and in
CC   chemotaxis. The polypeptides can also be used as a food additive or
CC   preservative to increase or decrease storage capabilities. AAF22364 to
CC   AAF22372 and AAB63133 represent sequences used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 1049 BP; 305 A; 242 C; 212 G; 288 T; 2 other;


  Query Match             3.6%;  Score 21;  DB 21;  Length 1049;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaaa 590
           |||||||||||||||||||||
Db      44 ATATTTAAAAAAAAAAAAAAA 24


RESULT  18
AAX20486
ID   AAX20486 standard; DNA; 1070 BP.
XX
AC   AAX20486;
XX
DT   04-MAY-1999  (first entry)
XX
DE   Human secreted protein gene 75.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
```

OS Homo sapiens.
XX
PN WO9906423-A1.
XX
PD 11-FEB-1999.
XX
PF 29-JUL-1998; 98WO-US15949.
XX
PR 19-AUG-1997; 97US-0056730.
PR 30-JUL-1997; 97US-0054209.
PR 30-JUL-1997; 97US-0054211.
PR 30-JUL-1997; 97US-0054212.
PR 30-JUL-1997; 97US-0054213.
PR 30-JUL-1997; 97US-0054214.
PR 30-JUL-1997; 97US-0054215.
PR 30-JUL-1997; 97US-0054217.
PR 30-JUL-1997; 97US-0054218.
PR 30-JUL-1997; 97US-0054234.
PR 30-JUL-1997; 97US-0054236.
PR 18-AUG-1997; 97US-0055968.
PR 18-AUG-1997; 97US-0055969.
PR 18-AUG-1997; 97US-0055972.
PR 19-AUG-1997; 97US-0056534.
PR 19-AUG-1997; 97US-0056543.
PR 19-AUG-1997; 97US-0056554.
PR 19-AUG-1997; 97US-0056561.
PR 19-AUG-1997; 97US-0056727.
PR 19-AUG-1997; 97US-0056729.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Carter KC, Endress GA, Fan P, Feng P, Kyaw H, Lafleur DW;
PI Li Y, Moore PA, Rosen CA, Ruben SM, Shi Y, Wei Y;
PI Zeng Z;
XX
DR WPI; 1999-153691/13.
DR P-PSDB; AAY00331.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 245; 312pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number is given in the descriptor line.
CC The gene can be used to generate fusion proteins by linking to the gene
CC to a human immunoglobulin Fc portion (e.g. AAX20403) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 83 novel genes and their fragments (nucleic
CC acid sequences: AAX20412-X20499; amino acid sequences AAY00258-Y00377)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 86
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAX20412 for described uses).
XX
SQ Sequence 1070 BP; 298 A; 258 C; 198 G; 313 T; 3 other;

Query Match 3.6%; Score 21; DB 20; Length 1070;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 570 atatttaaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 1019 atatttaaaaaaaaaaaaaaa 1039

RESULT 19
AAC93427

ID AAC93427 standard; cDNA; 1164 BP.
XX
AC AAC93427;
XX
DT 16-FEB-2001 (first entry)
XX
DE Human secreted protein gene 6 SEQ ID NO:16.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW opthalmalogical; vulnerary; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorders; cancer; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; nervous system disorder;
KW Alzheimer's disease; ocular disorder; wound healing; skin aging; ss.
XX
OS Homo sapiens.
XX
PN WO200061625-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US08981.
XX
PR 09-APR-1999; 99US-0128701.
PR 20-JAN-2000; 2000US-0177165.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-619225/59.
DR P-PSDB; AAB51730.
XX
PT New nucleic acid molecules encoding 48 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 1; Page 413; 500pp; English.
XX
CC Polynucleotide sequences AAC93422 - AAC93449 represent cDNA encoding
CC human secreted proteins AAB51724 - AAB51777. Sequences AAB51778 -
CC AAB51825 represent alternative polypeptides encoded by the genes, and
CC amino acid sequences to which they are homologous. The genes and proteins
CC have activities dependent on the tissues and cells in which they are
CC expressed. Examples of their activities include immunosuppressive;
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
CC virucide; fungicide; opthalmalogical; and vulnerary. The secreted
CC proteins, polynucleotides, antagonists and agonists may be useful in
CC treating, preventing and/or diagnosing diseases and disorders such as
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. Oligonucleotide AAC93413 - AAC93421 and peptide AAB51723 are
CC used in the isolation and characterisation of the proteins and
CC polynucleotides of the invention.
XX
SQ Sequence 1164 BP; 284 A; 269 C; 310 G; 301 T; 0 other;

Query Match 3.6%; Score 21; DB 21; Length 1164;
Best Local Similarity 100.0%; Pred. No. 33;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    570 atatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db   1144 atatttaaaaaaaaaaaaaa 1164
```

RESULT 20
AAC78079
ID AAC78079 standard; cDNA; 1279 BP.
XX
AC AAC78079;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated gene sequence SEQ ID NO:473.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening; ss.
XX
OS Homo sapiens.
XX
PN WO200055350-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05882.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587533/55.
DR P-PSDB; AAB43870.
XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer -
XX
PS Claim 1; Page 1008; 2352pp; English.
XX
CC AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerary; immunomodulator;
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1279 BP; 421 A; 226 C; 293 G; 337 T; 2 other;

Query Match 3.6%; Score 21; DB 21; Length 1279;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    570 atatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db   1222 atatttaaaaaaaaaaaaaa 1242
```

RESULT 21
AAH34582
ID AAH34582 standard; cDNA; 1279 BP.
XX
AC AAH34582;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1664.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 14; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG75177.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 3271; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 1279 BP; 421 A; 226 C; 294 G; 337 T; 1 other;

Query Match 3.6%; Score 21; DB 22; Length 1279;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    570 atatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db   1222 atatttaaaaaaaaaaaaaa 1242
```

```
RESULT 22
AAT17380
ID   AAT17380 standard; cDNA; 1302 BP.
XX
AC   AAT17380;
XX
DT   27-SEP-1996 (first entry)
XX
DE   DNA encoding endothelial cell protein receptor.
XX
KW   EPCR; endothelial cell protein C receptor; activated protein C;
KW   blood coagulation; inflammatory response; inhibit; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             25..741
FT                   /*tag= a
FT                   /product= endothelial_cell_protein_receptor
FT   sig_peptide     25..69
FT                   /*tag= b
FT   mat_peptide     70..738
FT                   /*tag= c
FT   polyA_signal    1267..1272
FT                   /*tag= d
XX
PN   WO9605303-A1.
XX
PD   22-FEB-1996.
XX
PF   09-AUG-1995;   95WO-US09636.
XX
PR   12-AUG-1994;   94US-0289699.
XX
PA   (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA   (OKLA-) OKLAHOMA MED RES FOUND.
XX
PI   Esmon CT, Fukudome K;
XX
DR   WPI; 1996-139699/14.
DR   P-PSDB; AAR81453.
XX
PT   Isolated endothelial cell protein C/activated protein C receptor -
PT   used to inhibit inflammatory responses, screen for cpds. which alter
PT   receptor binding and, by blocking receptor binding, enhance
PT   inflammatory response
XX
PS   Claim 1; Page 37-38; 58pp; English.
XX
CC   The present sequence encodes an endothelial cell protein C/activated
CC   protein C receptor (EPCR), a type I transmembrane glycoprotein. The
CC   protein binds with high affinity to both protein C (which plays a
CC   major role in blood coagulation) and activated protein C (Kd~30 nM)
CC   and is calcium dependent. It is a member of the CD1/MHC superfamily
CC   and has a role in regulating the inflammatory response.
XX
SQ   Sequence 1302 BP; 340 A; 325 C; 341 G; 296 T; 0 other;
```

```
  Query Match             3.6%;  Score 21;  DB 17;  Length 1302;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    570 atatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db   1279 atatttaaaaaaaaaaaaaa 1299
```

```
RESULT 23
AAV53733
ID   AAV53733 standard; cDNA; 1302 BP.
XX
AC   AAV53733;
XX
DT   20-NOV-1998 (first entry)
XX
DE   Nucelotide sequence of the endothelial cell protein receptor.
XX
KW   Human; endothelial cell protein receptor; inflammation; regulation;
KW   endothelial protein C receptor; EPCR; coagulation state; diabetes;
KW   major vascular condition; autoimmune disease; pre-eclampsia;
KW   cardiopulmonary bypass; unstable angina; restenosis; angioplasty;
KW   kidney disease; liver disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             25..741
FT                   /*tag= a
FT                   /product= "ECPR protein"
XX
PN   US5804392-A
XX
PD   08-SEP-1998
XX
PF   27-JUN-1997;   97US-0884203.
XX
PR   27-JUN-1997;   97US-0884203.
XX
PA   (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI   Esmon CT, Furosawa S, Stearns-Kurosawa DJ;
XX
DR   WPI; 1998-5 5645/43.
DR   P-PSDB; AAK24546.
XX
PT   Immuno-based detection of protein C receptor - useful in the
PT   diagnosis of inflammatory and coagulation states and disorders
PT   associated with damage to endothelium and large blood vessel disease
XX
PS   Disclosure; Columns 21-22; 23pp; English.
XX
CC   This is the nucleotide sequence of the human endothelial cell protein
CC   receptor, used in the method of the invention where endothelial protein
CC   C receptors (EPCR) is used in diagnosis of inflammatory and coagulation
CC   states and disorders associated with damage to endothelium and large
CC   blood vessel disease. ECPR is involved in the regulation of a host
CC   response to inflammation. The protein is one of the last components
CC   to be activated in the coagulation system, and is thought to control
CC   coagulation and inflammation. Activation of the receptor through a
CC   pathway involving thrombin, activates protein C. The protein C pathway
CC   is apparently only involved in large blood vessels, not capillaries,
CC   and so is activated with for major vascular conditions, and the
CC   increased presence of the receptor in the conditions stated makes it
CC   ideal as a diagnostic component. The assay is used for the diagnosis
CC   complications such as autoimmune diseases, pre-eclampsia, diabetes,
CC   vascular disease (especially cardiopulmonary bypass, unstable angina,
CC   restenosis and angioplasty), kidney disease and liver disease.
XX
SQ   Sequence 13 2 BP; 340 A; 325 C; 341 G; 296 T; 0 other;
```

```
  Query Match             3.6%;  Score 21;  DB 19;  Length 1302;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    570 atatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db   1279 atatttaaaaaaaaaaaaaa 1299
```

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RESULT 24
AAA07076
ID   AAA07076 standard; cDNA; 1302 BP.
XX
AC   AAA07076;
XX
DT   03-JUL-2000 (first entry)
XX
DE   cDNA encoding membrane-bound human endothelial protein C receptor (EPCR).
XX
KW   Endothelial protein C receptor; EPCR; membrane bound; splice variant;
KW   activated protein C; APC; coagulation; inflammation; regulation;
KW   endothelial cell; autoimmune disease; vascular damage; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             25..741
FT                   /*tag= a
FT                   /product= "Human membrane-bound EPCR splice variant"
FT   sig_peptide     25..69
FT                   /*tag= b
FT   mat_peptide     76..738
FT                   /*tag= c
FT                   /product= "Mature human membrane-bound EPCR"
FT   misc_feature    627..628
FT                   /*tag= d
FT                   /note= "Exon III-exon IV junction"
XX
PN   US6037450-A.
XX
PD   14-MAR-2000.
XX
PF   20-MAY-1998;   98US-0082021.
XX
PR   27-JUN-1997;   97US-0884203.
XX
PA   (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI   Stearns-Kurosawa DJ, Kurosawa S, Esmon CT;
XX
DR   WPI; 2000-246200/21.
DR   P-PSDB; AAY81476.
XX
PT   Modified endothelial protein C receptor, useful as diagnostic marker of
PT   e.g. inflammation or autoimmune diseases, is a soluble or alternatively
PT   spliced form of the receptor -
XX
PS   Claim 4; Columns 21-22; 24pp; English.
XX
CC   This sequence represents cDNA encoding the membrane-bound form of the
CC   human endothelial protein C receptor (EPCR). The invention relates to a
CC   modified form of EPCR, in which the C-terminal Cys of the membrane-
CC   bound form is not palmitoylated, or is otherwise replaced by a different
CC   amino acid; to a soluble splice variant of EPCR, which lacks a
CC   transmembrane domain; and to a EPCR in which the transmembrane domain
CC   of the membrane-bound form has been removed by proteolytic cleavage.
CC   Splicing of exon III to exon IV (which encodes the transmembrane domain)
CC   in the EPCR RNA transcript results in an mRNA encoding the
CC   membrane-bound form of the protein, while mRNA encoding the soluble form
CC   includes intron III sequences. The intron III sequence includes an
CC   in-frame termination codon; translation of intron III-containing mRNA
CC   results in an EPCR protein with a variant sequence (AAY81477) immediately
CC   C-terminal of glycine 201. EPCR binds both protein C and its activated
CC   form, activated protein C (APC), with similar affinity in the presence of
CC   calcium. The membrane-bound form facilitates protein C activation by
CC   presenting protein C to a thrombin/thrombomodulin activation complex on
CC   cell surfaces. In contrast, the soluble form inhibits protein C
CC   activation by competing with membrane-bound EPCR for protein C. The
CC   activation of protein C initiates a series of events that play a key role
CC   in the regulation of blood coagulation. Patients deficient in protein C
CC   usually exhibit life-threatening thrombotic complications in infancy.
CC   Protein C and APC are also involved in the regulation of the host
CC   response to inflammation. Measurement of soluble EPCR levels is used to
CC   diagnose disorders involving coagulation or inflammation, autoimmune
CC   diseases (e.g., lupus erythematosus), and conditions such as sepsis,
CC   diabetes, pre-eclampsia and restenosis. EPCR quantitation may be used
CC   for monitoring treatment, and may also be used to indicate damage to
CC   large blood vessels, as such damage stimulates proteolysis of endothelial
CC   cell membrane-bound EPCR, or the expression of the soluble EPCR splice
CC   variant. Anti-EPCR antibodies may also be used to characterise and
CC   isolate EPCR proteins and to modulate EPCR activity, particularly to
CC   inhibit ligand binding.
XX
SQ   Sequence 1302 BP; 340 A; 325 C; 341 G; 296 T; 0 other;

  Query Match             3.6%;  Score 21;  DB 21;  Length 1302;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db    1279 atatttaaaaaaaaaaaaaa 1299


RESULT 25
AAZ98076
ID   AAZ98076 standard; cDNA; 1373 BP.
XX
AC   AAZ98076;
XX
DT   09-MAY-2000 (first entry)
XX
DE   Human secreted protein encoding nucleotide sequence SEQ ID NO:70.
XX
KW   Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW   antiinflammatory; nootropic; neuroprotective; antiallergic; cancer;
KW   tumour; neurodegenerative disorder; developmental abnormality; allergy;
KW   foetal deficiency; blood disorder; immune system disorder; arthritis;
KW   autoimmune disease; hepatic disease; renal disease; inflammation;
KW   Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis;
KW   infection; AIDS; spinal cord injury; transplant rejection; diabetes;
KW   asthma; sepsis; acne; psoriasis; cardiovascular disorder;
KW   reproductive disorder; gastrointestinal disorder; respiratory disorder;
KW   metabolic disorder; food additive; preservative; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004140-A1.
XX
PD   27-JAN-2000.
XX
PF   14-JUL-1999;   99WO-US15849.
XX
PR   15-JUL-1998;   98US-0092921.
PR   15-JUL-1998;   98US-0092922.
PR   15-JUL-1998;   98US-0092956.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Komatsoulis G, Duan RD, Rosen CA, Moore PA, Shi Y;
PI   Lafleur DW, Ebner R, Olsen HS, Brewer LA, Florence KA, Young PE;
PI   Mucenski M, Endress GA, Soppet DR;
XX
DR   WPI; 2000-161128/14.
DR   P-PSDB; AAY87123.
XX
PI   New isolated human genes, useful for diagnosis and treatment of, e.g.
PT   cancers, neurological or blood disorders -
XX
PS   Claim 1; Page 346-347; 494pp; English.
XX
CC   The polynucleotide sequences given in AAZ98017 to AAZ98108 encode the
CC   human secreted proteins given in AAY87064 to AAY87223. Human secreted
```

CC protein can have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic;
CC immunosuppressive; antiinflammatory; nootropic; neuroprotective; and
CC antiallergic. The polynucleotides and their corresponding secreted
CC polypeptides are useful for preventing, treating or ameliorating medical
CC conditions, e.g. by protein or gene therapy. Also pathological conditions
CC can be diagnosed by determining the amount of the new polypeptides in a
CC sample or by determining the presence of mutations in the new
CC polynucleotides. Human secreted protein s and their polynucleotides can
CC be used for developing products for the diagnosis or treatment of cancer,
CC tumours, neurodegenerative disorders, developmental abnormalities and
CC foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation,
CC allergies, Alzheimer's disease, behavioural disorders, schizophrenia,
CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,
CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,
CC cardiovascular disorders, reproductive disorders, gastrointestinal
CC disorders, respiratory disorders and metabolic disorders. The
CC proteins or polynucleotides can also be used as food additives or
CC preservatives. The proteins are also useful for identifying their
CC binding partners. AAZ98008 to AAZ98016 and AAY87043 are sequence used in
CC the exemplification of the present invention.
XX
SQ Sequence 1373 BP; 325 A; 329 C; 361 G; 358 T; 0 other;

Query Match 3.6%; Score 21; DB 21; Length 1373;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 570 atatttaaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 1349 atatttaaaaaaaaaaaaaaa 1369

RESULT 26
AAD11689
ID AAD11689 standard; cDNA; 1373 BP.
XX
AC AAD11689;
XX
DT 21-SEP-2001 (first entry)
XX
DE Human secreted protein-encoding gene 60 cDNA clone HTACS12, SEQ ID NO:70.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnerary; binding partner identification;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 213..404
FT /tag= a
FT /product= "Human secreted protein precursor"
FT sig_peptide 213..299
FT /tag= b
FT mat_peptide 300..401
FT /tag= c
FT /product= "Mature human secreted protein"
XX
PN WO200151504-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US00311.

XX
PR 13-JAN-2000; 2000US-0482273.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Komatsoulis GA, Duan RR, Rosen CA, Moore PA, Shi Y;
PI Lafleur DW, Olsen HS, Brewer LA, Florence KA, Young PE, Soppet DR;
PI Endress GA, Muscenski M, Ebner R;
XX
DR WPI; 2001-425865/45.
DR P-PSDB; AAE05100.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 1; Page 713-714; 864pp; English.
XX
CC AAD11640-AAD11721 represent cDNAs corresponding to 71 human secreted
CC protein genes, and AAE06041 AAE06132 represent the proteins they encode.
CC AAE06133-AAE06205 represent human secreted protein fragments.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 71 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein-encoding cDNA of
CC the invention.
XX
SQ Sequence 1373 BP; 325 A; 329 C; 361 G; 358 T; 0 other;

Query Match 3.6%; Score 21; DB 22; Length 1373;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 570 atatttaaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 1349 atatttaaaaaaaaaaaaaaa 1369

RESULT 27
AAC91065
ID AAC91065 standard; DNA; 1547 BP.
XX
AC AAC91065;
XX
DT 19-MAR-2001 (first entry)
XX
DE Mouse ortholog of zsig81 DNA.
XX
KW Cytokine; zsig 81; wound healing; proliferation; differentiation;
KW migration; metabolism; ss.
XX
OS Mus musculus.

XX
PN WO200073459-A1.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15002.
XX
PR 01-JUN-1999; 99US-0323582.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Piddington CS, West JR, Holly RD, Burkhead SK;
XX
DR WPI; 2001-061540/07.
XX
PT New zsig81 polypeptides and polynucleotides useful for e.g. promoting
PT wound healing, or in diagnosing or treating disorders associated with
PT cell loss or abnormal cell proliferation, such as cancer -
XX
PS Disclosure; Page 95-96; 109pp; English.
XX
CC The present invention relates to zsig81 and fragments thereof. The
CC invention is useful for promoting wound healing, for modulating the
CC proliferation, differentiation, migration or metabolism of responsive
CC cell types that includes both primary and cultured cell lines, and for
CC stimulating the proliferation of cells expressing markers associated
CC with dendritic lineage cells.
XX
SQ Sequence 1547 BP; 428 A; 375 C; 357 G; 387 T; 0 other;

Query Match 3.6%; Score 21; DB 22; Length 1547;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 570 atatttaaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 1507 atatttaaaaaaaaaaaaaaa 1527

RESULT 28
AAD08465
ID AAD08465 standard; cDNA; 1549 BP.
XX
AC AAD08465;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human secreted protein-encoding gene 17 cDNA clone HHENZ15, SEQ ID NO:72.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnerary; binding partner identification;
KW gene therapy; chromosome 20; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 795..809
FT /*tag= a
FT /product= "Human secreted protein precursor"
FT /note= "Does not include start codon"
FT /partial
XX
PN WO200134643-A1.
XX
PD 17-MAY-2001.
XX
PF 08-NOV-2000; 2000WO-US30629.
XX
PR 12-NOV-1999; 99US-0164825.
PR 03-AUG-2000; 2000US-0222904.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Komatsoulis GA, Soppet DR, Shi Y;
XX
DR WPI; 2001-374441/39.
DR P-PSDB; AAE04160.
XX
PT Nucleic acids encoding 24 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating e.g. Gaucher's disease,
PT Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease,
PT diabetes mellitus and multiple sclerosis -
XX
PS Claim 1; Page 459-460; 532pp; English.
XX
CC AAD08404-AAD08478 represent cDNAs corresponding to 24 human secreted
CC protein genes, and AAE04100-AAE04170 represent the proteins they encode.
CC AAE04172-AAE04197 represent human-secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 24 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein-encoding cDNA of
CC the invention.
XX
SQ Sequence 1549 BP; 411 A; 302 C; 306 G; 529 T; 1 other;

Query Match 3.6%; Score 21; DB 22; Length 1549;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 570 atatttaaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 1513 atatttaaaaaaaaaaaaaaa 1533

RESULT 29
AAQ85984
ID AAQ85984 standard; cDNA to mRNA; 1624 BP.
XX
AC AAQ85984;
XX
DT 12-OCT-1995 (first entry)
XX
DE Oryza sativa pPFK-OS1 gene.
XX
KW ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme; plant;

```
KW   potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radish;
KW   Raphanus sativus; Flaveria brownii; primer; expression vector;
KW   Agrobacterium tumefaciens; sugar; storage; temperature; ds.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..1412
FT                   /*tag= a
FT                   /product= fructose-6-phosphate 1-phosphotransferase
FT   CDS             390..392
FT                   /*tag= b
FT                   /transl_except= seq: AAT, a.a.:Ile
XX
PN   WO9505457-A.
XX
PD   23-FEB-1995.
XX
PF   16-AUG-1994;   94WO-JP01352.
XX
PR   19-AUG-1993;   93JP-0226454.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Hiyoshi T,  Kasaoka K,  Mine T,  Page MJA,  Tyson HP;
XX
DR   WPI; 1995-098757/13.
DR   P-PSDB; AAR71581.
XX
PT   DNA coding for fructose-6-phosphate 1-phosphotransferase - of
PT   plant origin, for prodn. of transformant plant cells with altered
PT   sugar content
XX
PS   Claim 8; Page 46-49; 79pp; Japanese.
XX
CC   The sequences (AAQ85982-6) represent the genes encoding a novel
CC   ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme
CC   (EC 2.7.1.11; PFK) from a range of plants. This is the sequence of the
CC   Oryza sativa (rice) gene, pPFK-OS1, as given in the specification.
CC   Plants transformed with these genes can express the enzyme.  The
CC   transformed plants can produce varieties that have altered sugar content
CC   on storage at low temperatures.
XX
SQ   Sequence 1624 BP; 480 A; 302 C; 406 G; 436 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 16;  Length 1624;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    570 atatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db   1600 atatttaaaaaaaaaaaaaa 1620


RESULT  30
AAI58747
ID   AAI58747 standard; cDNA; 1763 BP.
XX
AC   AAI58747;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 950.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0633450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693035.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM39591.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 950; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1763 BP; 527 A; 327 C; 399 G; 510 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 22;  Length 1763;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    570 atatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db   1741 atatttaaaaaaaaaaaaaa 1761


RESULT  31
AAH48294
ID   AAH48294 standard; DNA; 1994 BP.
XX
AC   AAH48294;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Honeybee alpha-glucosidase coding sequence.
XX
KW   Honeybee; alpha-glucosidase; ds.
XX
OS   Apis mellifera.
XX
```

```
FH   Key             Location/Qualifiers
FT   CDS             13..1779
FT                   /*tag= a
FT                   /product= "alpha-glucosidase"
XX
PN   JP2001136986-A.
XX
PD   22-MAY-2001.
XX
PF   01-SEP-2000; 2000JP-0265070.
XX
PR   01-SEP-1999;  99JP-0246862.
XX
PA   (NISO ) NIPPON SHOKUHIN KAKO KK.
XX
DR   WPI; 2001-460212/50.
DR   P-PSDB; AAG64875.
XX
PT   Apis mellifera alpha-glucosidase gene -
XX
PS   Claim 2; Page 6-9; 11pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences of the
CC   honeybee alpha-glucosidase. The gene can be used for the preparation of
CC   Apis mellifera alpha-glucosidase I. The present sequence is the coding
CC   sequence of the invention.
XX
SQ   Sequence 1994 BP; 753 A; 310 C; 357 G; 574 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 22;  Length 1994;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db    1915 atatttaaaaaaaaaaaaaa 1935


RESULT  32
AAZ33647
ID   AAZ33647 standard; cDNA; 2281 BP.
XX
AC   AAZ33647;
XX
DT   08-DEC-1999  (first entry)
XX
DE   Human breast tumour-associated EST 37.
XX
KW   Expressed sequence tag; EST; human; breast; cancer; gene therapy;
KW   treatment; tumour; cytostatic; medicament; ss.
XX
OS   Homo sapiens.
XX
PN   DE19813839-A1.
XX
PD   23-SEP-1999.
XX
PF   20-MAR-1998;  98DE-1013839.
XX
PR   20-MAR-1998;  98DE-1013839.
XX
PA   (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI   Specht T,  Hinzmann B,  Schmitt A,  Pilarsky C,  Dahl E,  Rosentahl A;
XX
DR   WPI; 1999-528981/45.
DR   P-PSDB; AAY48573.
XX
PT   Human nucleic acid sequences and protein products from tumor breast
PT   tissue, useful for breast cancer therapy -
XX
PS   Claim 1a; 116-117; 188pp; German.
XX
CC   This invention describes novel human nucleic acid sequences from tumor
CC   breast tissue which have cytostatic activity. The nucleic acid sequences
CC   can be used to produce and isolate full-length gene sequences. They can
CC   be used to express proteins, which can be used as tools to find an
CC   activity against breast cancer. The sequences can be used in sense or
CC   antisense form. They are especially useful for medicaments for gene
CC   therapy to treat breast cancer. AAZ33611-Z48617 represents expressed
CC   sequence tags described in the method of the invention.
XX
SQ   Sequence 2281 BP; 601 A; 498 C; 494 G; 688 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 20;  Length 2281;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db    2248 atatttaaaaaaaaaaaaaa 2268


RESULT  33
AAQ90652
ID   AAQ90652 standard; cDNA; 3133 BP.
XX
AC   AAQ90652;
XX
DT   11-NOV-1995  (first entry)
XX
DE   Eph-related tyrosine kinase CEK6 cDNA.
XX
KW   Cek6; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
KW   prognosis; ss.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..419
FT                   /*tag= a
FT   CDS             421..2859
FT                   /*tag= b
XX
PN   WO9515375-A.
XX
PD   08-JUN-1995.
XX
PF   07-SEP-1994;  94WO-US10140.
XX
PR   03-DEC-1993;  93US-0162809.
XX
PA   (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI   Pasquale EB,  Sajjadi FG;
XX
DR   WPI; 1995-215256/28.
DR   P-PSDB; AAR75704.
XX
PT   Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT   cancer.
XX
PS   Disclosure; Page 37-41; 129pp; English.
XX
CC   Novel EPH-related PTK Cek6 cDNA clones (AAQ90652) were isolated from
CC   chick embryo and embryonic brain cDNA libraries in phage lambda gt11.
CC   The encoded Cek6 protein (AAR75704) is closely related to rat Elk,
CC   Cek5 (AAR75712) and Cek10 (AAR75708). Cek6 transcripts were found in
CC   10-day embryos and in adult brain, lung, heart and skeletal muscle.
XX
SQ   Sequence 3133 BP; 718 A; 918 C; 922 G; 575 T; 0 other;


  Query Match             3.6%;  Score 21;  DB 16;  Length 3133;
```

```
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db    3108 atatttaaaaaaaaaaaaaa 3128


RESULT  34
AAH19355
ID   AAH19355 standard; cDNA; 3831 BP.
XX
AC   AAH19355;
XX
DT   25-JUL-2001  (first entry)
XX
DE   Porcine CD29 protein coding sequence.
XX
KW   Porcine; CD29; immunosuppressive; immunomodulatory;
KW   epitope Gal-alpha-(1,3)-Gal; xenotransplantation; xenograft; ss.
XX
OS   Sus scrofa.
XX
FH   Key             Location/Qualifiers
FT   CDS             241..2637
FT                   /*tag= a
FT                   /product= "Porcine CD49"
FT                   /transl_except= "(pos:1027..1035,aa:Ser-Leu-Ile)"
XX
PN   WO200125279-A1.
XX
PD   12-APR-2001.
XX
PF   04-OCT-2000; 2000WO-ES00374.
XX
PR   05-OCT-1999;   99ES-0002193.
XX
PA   (BIOV-) BIOVET-UCO SL.
XX
PI   Garrido Pavon JJ,  Llanes Ruiz D,  Babancho Medina M;
PI   Jimenez Marin AM;
XX
DR   WPI; 2001-273569/28.
DR   P-PSDB; AAB84751.
XX
PT   Porcine CD29 protein and related DNA, useful for removing xenoreactive
PT   antibodies to prevent graft rejection and to prepare transgenic animals
PT   useful as graft donors -
XX
PS   Claim 4; Page 38-39; 46pp; Spanish.
XX
CC   The present sequence is the coding sequence for porcine CD29 protein.
CC   CD29 contains epitopes Gal-alpha-(1,3)-Gal, which are recognised by
CC   xenoreactive human antibodies, leading to hyperacute rejection of
CC   xenografts. The present invention relates to CD29 proteins, which have an
CC   identical, reduced or zero expression of epitope Gal-alpha-(1,3)-Gal,
CC   which can be used to reduce or prevent hyperacute rejection associated
CC   with xenotransplantation.
XX
SQ   Sequence 3831 BP; 1114 A; 703 C; 920 G; 1094 T; 0 other;

  Query Match             3.6%;  Score 21;  DB 22;  Length 3831;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db    3808 atatttaaaaaaaaaaaaaa 3828


RESULT  35
AAX39681/c
ID   AAX39681 standard; DNA; 5306 BP.
XX
AC   AAX39681;
XX
DT   02-JUL-1999  (first entry)
XX
DE   Renal cancer associated gene.
XX
KW   Cancer associated antigen; diagnosis; research; treatment; human;
KW   breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW   prostate cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9904265-A2.
XX
PD   28-JAN-1999.
XX
PF   15-JUL-1998;   98WO-US14679.
XX
PR   22-JUN-1998;   98US-0102322.
PR   17-JUL-1997;   97US-0896164.
PR   10-OCT-1997;   97US-0061599.
PR   10-OCT-1997;   97US-0061765.
PR   10-OCT-1997;   97US-0948705.
PR   11-OCT-1997;   97GB-0021697.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Chen Y,  Gout I,  Gure A,  O'Hare M,  Obata Y,  Old LJ;
PI   Pfreundschuh M,  Sahin U,  Scanlan MJ,  Stockert E;
PI   Tureci O;
XX
DR   WPI; 1999-132448/11.
XX
PT   New isolated cancer associated nucleic acids and polypeptides -
PT   isolated using sera from cancer patients, used to develop products
PT   for the diagnosis, monitoring or treatment of cancers
XX
PS   Claim 67; Page 500-502; 787pp; English.
XX
CC   The invention relates to a method for diagnosing a disorder characterised
CC   by expression of a human cancer associated antigen precursor coded for by
CC   a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC   biological sample isolated from a subject with an agent that specifically
CC   binds to the NAM, an expression product or a fragment of an expression
CC   product complexed with an HLA molecule; and (b) determining the
CC   interaction between the agent and the NAM or the expression product as a
CC   determination of the disorder. The products and methods can be used in
CC   the diagnosis, monitoring, research, or treatment of conditions
CC   characterised by the expression of various cancer associated antigens.
CC   The invention provides nucleic acid sequences and encoded polypeptides
CC   which are cancer associated antigen precursors expressed in human breast
CC   cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC   lung cancer.
XX
SQ   Sequence 5306 BP; 1867 A; 973 C; 1076 G; 1390 T; 0 other;

  Query Match             3.6%;  Score 21;  DB 20;  Length 5306;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     570 atatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db    1100 ATATTTAAAAAAAAAAAAAA 1080


RESULT  36
AAN50530/c
ID   AAN50530 standard; DNA; 5750 BP.
XX
AC   AAN50530;
```

XX
DT 30-SEP-1991 (first entry)
XX
DE Sequence encoding the P195 protein of Plasmodium falciparum.
XX
KW Malaria vaccine; epitope; antigen; immunogen; ss.
XX
OS Plasmodium falciparum.
XX
FH Key Location/Qualifiers
FT CDS 216..5179
FT /*tag= a
XX
PN EP154454-A.
XX
PD 11-SEP-1985.
XX
PF 21-FEB-1985; 85EP-0301173.
XX
PR 26-SEP-1984; 84GB-0024340.
PR 22-FEB-1984; 84GB-0004692.
PR 21-FEB-1985; 85GB-0004429.
XX
PA (WELL) WELLCOME FOUNDATION LTD.
XX
PI Holder A, Sandhu J, Odink K, Lockyer M, Riveros-Moreno V;
XX
DR WPI; 1985-224845/37.
DR P-PSDB; AAP50777.
XX
PT Cloned DNA sequence encoding plasmodium falciparum protein -
PT useful for expressing the protein for use in vaccines against
PT malaria
XX
PS Claim 2; Fig 1; 51pp; English.
XX
CC The sequence encoding the P195 protein of Plasmodium falciparum
CC (AAN50530) and a peptide comprising at least one of its epitopes
CC (see AAP50777) are claimed. Also claimed is a vaccine for inducing
CC immunity to malaria comprising the novel peptide or P195 or a
CC peptide comprising at least one epitope when derived from the new
CC DNA sequence, together with a carrier.
XX
SQ Sequence 5760 BP; 2565 A; 630 C; 725 G; 1840 T; 0 other;

Query Match 3.6%; Score 21; DB 6; Length 5760;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 570 atatttaaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 5240 ATATTTAAAAAAAAAAAAAAA 5220

RESULT 37
AAC77811
ID AAC77811 standard; cDNA; 5830 BP.
XX
AC AAC77811;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated gene sequence SEQ ID NO:205.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening; ss.
XX
OS Homo sapiens.
XX
PN WO200055350-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05882.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587533/55.
DR P-PSDB; AAB43602.
XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer -
XX
PS Claim 1; Page 777-779; 2352pp; English.
XX
CC AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerary; immunomodulator;
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 5830 BP; 1558 A; 1417 C; 1409 G; 1439 T; 7 other;

Query Match 3.6%; Score 21; DB 21; Length 5830;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 570 atatttaaaaaaaaaaaaaaa 590
||||||||||||||||||||||
Db 5762 atatttaaaaaaaaaaaaaaa 5782

RESULT 38
AAX76366/c
ID AAX76366 standard; DNA; 35 BP.
XX
AC AAX76366;
XX
DT 05-AUG-1999 (first entry)
XX
DE Pneumocystis carinii lysyl-tRNA synthetase PCR primer #29.
XX
KW Pneumocystis carinii; lysyl-tRNA synthetase; tyrosyl-tRNA synthetase;
KW aminoacyl-tRNA synthetase; pneumonia; AIDS; immuno-compromised;
KW Acquired Immune Deficiency Syndrome; detection; PCR primer; ss.
XX

```
OS   Synthetic.
OS   Pneumocystis carinii.
XX
PN   US5912140-A.
XX
PD   15-JUN-1999.
XX
PF   03-APR-1995;   95US-0415593.
XX
PR   03-APR-1995;   95US-0415593.
XX
PA   (CUBI-) CUBIST PHARM INC.
XX
PI   Politis-Virk KI,  Quinn CL,  Schimmel PR,  Tao N,  Whoriskey SK;
XX
DR   WPI; 1999-357196/30.
XX
PT   Nucleic acids encoding Pneumocystis carinii aminoacyl-tRNA
PT   synthetase enzymes useful for detecting similar sequences in samples
PT   and in the study and treatment of pneumonia in Acquired Immune
PT   Deficiency Syndrome patients
XX
PS   Example 17; Column 47; 66pp; English.
XX
CC   The present invention describes Pneumocystis carinii (P. carinii)
CC   aminoacyl-tRNA synthetase enzymes. The nucleic acids encoding aminoacyl-
CC   tRNA synthetase enzymes may be used to produce expression vectors and
CC   host cells for the recombinant production of Pneumocystis aminoacyl-tRNA
CC   synthetases. The proteins may then be used in other procedures such as
CC   separating amino acids from samples or as antigens in the production of
CC   antibodies. The nucleic acids may also be used to produce tester cell
CC   strains (which contain the nucleic acids) which may be used to test
CC   candidate drugs (e.g. tRNA synthetase inhibitors) for the treatment of
CC   disorder associated with P. carinii such as pneumonia which is a common
CC   complication for Acquired Immune Deficiency Syndrome (AIDS) patients and
CC   other immuno-compromised individuals. Additionally, they may also be
CC   used to detect and isolate related DNAs in sample (i.e. they can be used
CC   as probes). The present sequence represents a PCR primer for a
CC   Pneumocystis aminoacyl-tRNA synthetase, used in an example from the
CC   present invention.
XX
SQ   Sequence 35 BP; 7 A; 5 C; 2 G; 21 T; 0 other;


  Query Match             3.4%;  Score 20;  DB 20;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    571 tatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db     30 TATTTAAAAAAAAAAAAAA 11


RESULT  39
AAX76360/c
ID   AAX76360 standard; DNA; 40 BP.
XX
AC   AAX76360;
XX
DT   05-AUG-1999  (first entry)
XX
DE   Pneumocystis carinii lysyl-tRNA synthetase PCR primer 33.
XX
KW   Pneumocystis carinii; lysyl-tRNA synthetase; tyrosyl-tRNA synthetase;
KW   aminoacyl-tRNA synthetase; pneumonia; AIDS; immuno-compromised;
KW   Acquired Immune Deficiency Syndrome; detection; PCR primer; ss.
XX
OS   Synthetic.
OS   Pneumocystis carinii.
XX
PN   US5912140-A.
XX
PD   15-JUN-1999.
XX
PF   03-APR-1995;   95US-0415593.
XX
PR   03-APR-1995;   95US-0415593.
XX
PA   (CUBI-) CUBIST PHARM INC.
XX
PI   Politis-Virk KI,  Quinn CL,  Schimmel PR,  Tao N,  Whoriskey SK;
XX
DR   WPI; 1999-357196/30.
XX
PT   Nucleic acids encoding Pneumocystis carinii aminoacyl-tRNA
PT   synthetase enzymes useful for detecting similar sequences in samples
PT   and in the study and treatment of pneumonia in Acquired Immune
PT   Deficiency Syndrome patients
XX
PS   Example 16; Column 44; 66pp; English.
XX
CC   The present invention describes Pneumocystis carinii (P. carinii)
CC   aminoacyl-tRNA synthetase enzymes. The nucleic acids encoding aminoacyl-
CC   tRNA synthetase enzymes may be used to produce expression vectors and
CC   host cells for the recombinant production of Pneumocystis aminoacyl-tRNA
CC   synthetases. The proteins may then be used in other procedures such as
CC   separating amino acids from samples or as antigens in the production of
CC   antibodies. The nucleic acids may also be used to produce tester cell
CC   strains (which contain the nucleic acids) which may be used to test
CC   candidate drugs (e.g. tRNA synthetase inhibitors) for the treatment of
CC   disorder associated with P. carinii such as pneumonia which is a common
CC   complication for Acquired Immune Deficiency Syndrome (AIDS) patients and
CC   other immuno-compromised individuals. Additionally, they may also be
CC   used to detect and isolate related DNAs in sample (i.e. they can be used
CC   as probes). The present sequence represents a PCR primer for a
CC   Pneumocystis aminoacyl-tRNA synthetase, used in an example from the
CC   present invention.
XX
SQ   Sequence 40 BP; 8 A; 6 C; 4 G; 22 T; 0 other;


  Query Match             3.4%;  Score 20;  DB 20;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    571 tatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db     35 TATTTAAAAAAAAAAAAAA 16


RESULT  40
AAT17027/c
ID   AAT17027 standard; DNA; 42 BP.
XX
AC   AAT17027;
XX
DT   04-OCT-1996  (first entry)
XX
DE   Human mitochondrial DNA heavy chain primer H16070.
XX
KW   Human; mitochondrial DNA; heavy chain; primer; polymorphism;
KW   identification; discrete single nucleotide bases; method; screen;
KW   genetic disease; DNA typing; forensic testing; microorganisms; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..17
FT                   /*tag= a
FT                   /note= "5'-polyT tail, opt. polyA"
XX
PN   WO9606187-A1.
XX
PD   29-FEB-1996.
XX
PF   21-AUG-1995;   95WO-GB01987.
```

```
XX
PR   25-AUG-1994;   94GB-0017211.
XX
PA   (SOLI-) SOLICITOR AFFAIRS OF HM TREASURY.
XX
PI   Sullivan K.  Tully G;
XX
DR   WPI; 1996-151390/15.
XX
PT   Identifying single nucleotide bases adjacent to target sequence
PT   by annealing primer adjacent to the base and extension with
PT   fluorescently labelled chain terminator, for simultaneous screening
PT   of genetic diseases, or for forensic testing
XX
PS   Claim 21; Page 18; 40pp; English.
XX
CC   The present oligonucleotide is the human mitochondrial DNA heavy
CC   chain primer AAH16070, where the No. is the position adjacent to the
CC   polymorphism to which the primer end base binds. The primer is
CC   used in a claimed method for the identification of at least 2
CC   discrete, single nucleotide bases (nb), each adjacent to a target
CC   sequence in a polynucleotide chain.
CC   A sample is mixed with primers (P) that are complementary to the
CC   characterised base sequence so that they anneal to the nb, at
CC   least 2 types of chain terminator each having a characteristic
CC   fluorescent label, and a chain extending enzyme so that the
CC   terminators complementary to the nb are incorporated into P. The
CC   extended P are then sepd. according to size or charge, and the
CC   terminator incorporated identified. The method can be used to
CC   screen for genetic diseases associated with single nb, and for DNA
CC   typing, e.g. in forensic testing, it may also be used to screen
CC   microorganisms.
XX
SQ   Sequence 42 BP; 7 A; 2 C; 8 G; 25 T; 0 other;


  Query Match             3.4%;  Score 20;  DB 17;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    571 tatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db     22 TATTTAAAAAAAAAAAAAA 3


RESULT  41
AAA61354
ID   AAA61354 standard; mRNA; 51 BP.
XX
AC   AAA61354;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Model mRNA #3 used to demonstrate DNA-protein fusion.
XX
KW   DNA-protein fusion; RNA-protein fusion; stable; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    6..28
FT                   /*tag= a
FT                   /bound_moiety= "Linker 7"
XX
PN   WO200032823-A1.
XX
PD   08-JUN-2000.
XX
PF   02-DEC-1999;   99WO-US28472.
XX
PR   02-DEC-1998;   98US-0110549.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Lohse P,  Kurz M,  Wagner R;
XX
DR   WPI: 2000-412359/35.
XX
PT   Generating a DNA-protein fusion useful for selecting a desired protein
PT   or the encoding DNA, comprises covalently linking proteins with their
PT   encoding DNA sequences
XX
PS   Disclosure; Fig 14; 51pp; English.
XX
CC   The present invention relates to methods of covalently tagging proteins
CC   with their encoding DNA sequences. Several methods may be used to create
CC   these DNA-protein fusions. In general, the methods involve linking a
CC   primer to an RNA molecule, then translating the RNA to produce a protein
CC   which is bound to the primer. The RNA is then reverse transcribed to
CC   give a DNA-protein fusion. The present sequence is model mRNA #3
CC   that was used to demonstrate DNA-protein fusion formation. This
CC   sequence was used as a substrate for the binding of linker 7 (see
CC   AAA61351). The DNA-protein fusions are useful in binding and molecular
CC   recognition assays that involve biological materials containing
CC   ribonucleases. The covalent bond between the protein and the encoding
CC   DNA makes the fusion more stable than RNA-protein fusions. This means
CC   selection experiments need not be limited to extremely mild reaction
CC   conditions.
XX
SQ   Sequence 51 BP; 26 A; 7 C; 6 G; 7 U; 5 other;


  Query Match             3.4%;  Score 20;  DB 21;  Length 51;
  Best Local Similarity   80.0%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    571 tatttaaaaaaaaaaaaaa 590
          :|:::|||||||||||||||
Db     27 uauuuaaaaaaaaaaaaaa 46


RESULT  42
AAV26706
ID   AAV26706 standard; cDNA; 79 BP.
XX
AC   AAV26706;
XX
DT   11-SEP-1998  (first entry)
XX
DE   Human novel secreted protein clone BF290_1i 3'-end DNA.
XX
KW   Secreted protein; human; marker; cytokine; immune stimulant; suppressor;
KW   autoimmune disease; regulator; activin; inhibin; inhibitor; chemotactic;
KW   chemokinetic; haemostatic; thrombocyte; tumour; anti-inflammatory; ds.
XX
OS   Homo sapiens.
XX
PN   WO9814470-A2.
XX
PD   09-APR-1998.
XX
PF   03-OCT-1997;   97WO-US18032.
XX
PR   04-OCT-1996;   96US-0725885.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D,  Racie LA;
PI   Spaulding V,  Treacy M;
XX
DR   WPI: 1998-240017/21.
XX
PI   Compositions containing isolated proteins encoded by specific
PT   nucleic acids - useful e.g. as anti-inflammatory, immune stimulant
PT   or suppressor, etc.
XX
```

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PS   Disclosure; Page 94; 117pp; English.
XX
CC   This sequence encodes the 3'-end of a novel secreted protein from clone
CC   BF290_11 isolated from a human fetal brain cDNA library. Such secreted
CC   proteins can be used for, e.g. research purposes (as markers for
CC   tissues, molecular weight markers for gels, primers and probes), for
CC   nutrition (as C, N or carbohydrate source), as a cytokine for cell
CC   proliferation and differentiation activity, as immune stimulants or
CC   suppressors, e.g. for viral, bacterial or fungal infections, for
CC   autoimmune diseases such as multiple sclerosis or systemic lupus
CC   erythematosus, to regulate haematopoiesis, for tissue growth, as an
CC   activin or inhibin, or having chemotactic or chemo-kinetic, haemostatic
CC   and thrombocytic, receptor/ligand, anti-inflammatory or tumour inhibitory
CC   activities.
XX
SQ   Sequence 79 BP; 73 A; 0 C; 0 G; 6 T; 0 other;


  Query Match             3.4%;  Score 20;  DB 19;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     571 tatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db       3 tatttaaaaaaaaaaaaaa 22


RESULT  43
AAA61347
ID   AAA61347 standard; RNA; 115 BP.
XX
AC   AAA61347;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Model RNA substrate #3 used to demonstrate DNA-protein fusion.
XX
KW   DNA-protein fusion; RNA-protein fusion; stable; ss.
XX
OS   Synthetic.
XX
PN   WO200032823-A1.
XX
PD   08-JUN-2000.
XX
PF   02-DEC-1999;   99WO-US28472.
XX
PR   02-DEC-1998;   98US-0110549.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Lohse P,  Kurz M,  Wagner R;
XX
DR   WPI; 2000-412359/35.
XX
PT   Generating a DNA-protein fusion useful for selecting a desired protein
PT   or the encoding DNA, comprises covalently linking proteins with their
PT   encoding DNA sequences -
XX
PS   Disclosure; Page 15; 51pp; English.
XX
CC   The present invention relates to methods of covalently tagging proteins
CC   with their encoding DNA sequences. Several methods may be used to create
CC   these DNA-protein fusions. In general, the methods involve linking a
CC   primer to an RNA molecule, then translating the RNA to produce a protein
CC   which is bound to the primer. The RNA is then reverse transcribed to
CC   give a DNA-protein fusion. The present sequence is model RNA substrate
CC   #3 that was used to demonstrate DNA-protein fusion formation. The
CC   DNA-protein fusions are useful in binding and molecular recognition
CC   assays that involve biological materials containing ribonucleases. The
CC   covalent bond between the protein and the encoding DNA makes the
CC   fusion more stable than RNA-protein fusions. This means selection
CC   experiments need not be limited to extremely mild reaction conditions.
XX
SQ   Sequence 115 BP; 48 A; 23 C; 23 G; 21 U; 0 other;


  Query Match             3.4%;  Score 20;  DB 21;  Length 115;
  Best Local Similarity   80.0%;  Pred. No. 1e+02;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     571 tatttaaaaaaaaaaaaaa 590
           :|:::|||||||||||||||
Db      91 uauuuaaaaaaaaaaaaaa 110


RESULT  44
AAA31926/c
ID   AAA31926 standard; DNA; 242 BP.
XX
AC   AAA31926;
XX
DT   05-JUL-2000  (first entry)
XX
DE   Plant microsatellite marker #887.
XX
KW   Plant microsatellite sequence; core repeat sequence; detection; probe;
KW   DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KW   variety identification; genetic variability evaluation; primer; ss.
XX
OS   Eucalyptus grandis.
XX
PN   WO9967421-A1.
XX
PD   29-DEC-1999.
XX
PF   25-JUN-1999;   99WO-NZ00092.
XX
PR   25-JUN-1998;   98US-0105307.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
PA   (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI   Havukkala II,  Bloksberg LN,  Glenn M;
XX
DR   WPI; 2000-116958/10.
XX
PT   New plant microsatellite markers and associated flanking species for
PT   the detection of polymorphic genetic markers -
XX
PS   Claim 1; Page 337; 392pp; English.
XX
CC   Sequences AAA31040-A32093 represent novel plant microsatellite sequences
CC   and associated flanking species. The sequences comprise a central core
CC   repeat sequence, especially selected from the sequences AAA32094-A32096
CC   with left and right flanking sequences. The polynucleotide sequences
CC   can be used in the detection of DNA polymorphisms, in genome mapping,
CC   in physical mapping, in positional cloning of genes, in variety
CC   identification and in evaluation of genetic variability within and
CC   between plant tissues, populations, cultivars, species and species
CC   groups. They may also be used to design hybridization probes for
CC   oligonucleotide fingerprinting and library screening and to design
CC   primers for microsatellite-primed PCR. Microsatellite markers are
CC   useful to locate specific economically useful genes in plant genomes.
XX
SQ   Sequence 242 BP; 106 A; 23 C; 70 G; 43 T; 0 other;


  Query Match             3.4%;  Score 20;  DB 21;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     571 tatttaaaaaaaaaaaaaa 590
           ||||||||||||||||||||
Db     119 TATTTAAAAAAAAAAAAAA 100
```

```
RESULT 45
AAZ08301
ID   AAZ08301 standard; cDNA; 278 BP.
XX
AC   AAZ08301;
XX
DT   13-OCT-1999  (first entry)
XX
DE   Human lung tumour protein SAL-109 5' cDNA sequence.
XX
KW   Human; lung tumour protein; therapy; diagnosis; lung cancer; vaccine;
KW   immunotherapy; detection; inhibition; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938973-A2.
XX
PD   05-AUG-1999.
XX
PF   26-JAN-1999;   99WO-US01642.
XX
PR   22-DEC-1998;   98US-0219245.
PR   28-JAN-1998;   98US-0015022.
PR   28-JAN-1998;   98US-0015029.
PR   18-MAR-1998;   98US-0040828.
PR   18-MAR-1998;   98US-0040831.
PR   23-JUL-1998;   98US-0122191.
PR   23-JUL-1998;   98US-0122192.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Frudakis TN,  Lodes MJ,  Mohamath R,  Reed SG;
XX
DR   WPI; 1999-479187/40.
XX
PT   Lung tumour specific polynucleotides for inhibiting the development
PT   of lung cancer
XX
PS   Claim 13; Page 139; 171pp; English.
XX
CC   The present invention describes lung tumour specific polynucleotides
CC   and tumour antigens. AAZ07144 to AAZ07246 and AAZ08301 to AAZ08325
CC   represent specifically claimed polynucleotides, and AAY29486 to AAY29571
CC   represent amino acid sequences from the present invention. The lung
CC   tumour specific polynucleotides and polypeptides can be used in
CC   pharmaceutical compositions and vaccines to inhibit the development of
CC   lung cancer. They can also be used to detect lung cancer in a patient.
CC   Probes and antibodies derived from the lung tumour sequences are useful
CC   in detection of lung cancer.
XX
SQ   Sequence 278 BP; 113 A; 41 C; 45 G; 79 T; 0 other;


  Query Match             3.4%;  Score 20;  DB 20;  Length 278;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    571 tatttaaaaaaaaaaaaaa 590
          ||||||||||||||||||||
Db     30 tatttaaaaaaaaaaaaaa 49


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Job time: 12217 sec
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GenSeqre version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 30, 2002, 10:54:22 ; Search time 728.83 Seconds
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Perfect score: 1079
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 10

Total number of hits satisfying chosen parameters: 420874

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	1079	100.0	1079	20	AAX84209	DNA encoding human
	2	1079	100.0	1079	21	AAC79438	cDNA sequence of h
c	3	959	88.9	1948	22	AAI58997	Human polynucleoti
c	4	959	88.9	1958	22	AAI60783	Human polynucleoti
c	5	908	84.2	1920	21	AAZ47118	Human CD40 recepto
c	6	908	84.2	2499	20	AAX28153	Topoisomerase II b
c	7	799	74.1	1898	22	AAH15146	Human cDNA sequenc
c	8	501	46.4	1296	21	AAC98160	Human colon cancer
c	9	209	19.4	752	22	AAH08073	Human cDNA clone (
c	10	94	8.7	444	22	AAI15311	Probe #5244 for ge
c	11	94	8.7	691	22	AAI24484	Probe #14417 for g
c	12	80	7.4	483	20	AAX40590	Human secreted pro
	13	47	4.4	47	21	AAZ68596	Human map-related
	14	45	4.2	579	22	AAH13035	Human cDNA clone (
c	15	36	3.3	1312	21	AAZ47119	Mouse CD40 recepto
	16	21	1.9	417	22	AAH33140	Human colon cancer
	17	21	1.9	5232	19	AAV55038	Human XIAP coding
	18	20	1.9	237	21	AAC31359	Human secreted pro
c	19	20	1.9	577	21	AAC34438	Arabidopsis thalia
c	20	20	1.9	960	21	AAC44257	Arabidopsis thalia
c	21	19	1.8	19	21	AAZ76456	Human biallelic ma
	22	19	1.8	338	22	AAH69026	Human cervical can
	23	19	1.8	351	22	AAH71896	Human cervical can
	24	19	1.8	494	22	AAH70685	Human cervical can
c	25	19	1.8	494	22	AAH72662	Human cervical can
	26	19	1.8	861	20	AAX22252	Human secreted pro
	27	19	1.8	1864	8	AAN71405	Sequence of ANS-1
	28	19	1.8	1864	15	AAQ78892	Aspergillus nidula
c	29	19	1.8	2438	22	AAF92529	Rat T2R02 nucleoti
c	30	19	1.8	2706	22	AA159313	Human polynucleoti
c	31	19	1.8	4605	20	AAX13252	Enterococcus faeca
	32	18	1.7	291	22	AAH33754	Human colon cancer
	33	18	1.7	1361	20	AAX02970	Human IL-1ra BAC c
	34	18	1.7	1569	21	AAC75762	Human ORFX ORF1317
c	35	18	1.7	1752	13	AAQ22695	Sequence encoding
c	36	18	1.7	1923	13	AAQ23258	Mitochondrial NAD(
c	37	18	1.7	2033	21	AAF18038	Lung cancer associ
c	38	18	1.7	3060	12	AAQ13822	Human GAP b3 gene.
c	39	18	1.7	4636	19	AAV23920	Human alpha3 integ
c	40	18	1.7	41708	21	AAA68247	Bacteriophage 77 c
c	41	18	1.7	41708	22	AAC86106	Complete genome of
	42	17	1.6	212	21	AAC31204	Human secreted pro
	43	17	1.6	314	21	AAC10599	Human secreted pro
	44	17	1.6	329	22	AAH71986	Human cervical can
c	45	17	1.6	396	21	AAC54948	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAX84209
ID AAX84209 standard; cDNA; 1079 BP.
XX
AC AAX84209;
XX
DT 08-SEP-1999 (first entry)
XX
DE DNA encoding human breast tumour protein immunogenic fragment.
XX
KW Breast tumour protein; immunogenic fragment; vaccine; detection;
KW breast cancer development; therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9933869-A2.
XX
PD 08-JUL-1999.
XX
PF 22-DEC-1998; 98WO-US27416.
XX
PR 17-JUL-1998; 98US-0118627.
PR 24-DEC-1997; 97US-0998253.
PR 24-DEC-1997; 97US-0998255.
PR 17-JUL-1998; 98US-0118554.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J;
XX
DR WPI; 1999-405486/34.
XX
PT New breast tumour protein genes used, in vaccines for immunotherapy,
PT or for diagnosis of breast cancer

```
XX
PS   Claim 3; Page 60; 70pp; English.
XX
CC   This sequence encodes a human breast tumour protein immunogenic fragment
CC   of the invention. The polypeptides or nucleic acids encoding them are
CC   useful in vaccines and pharmaceutical compositions for manufacture of
CC   medicaments for inhibiting the development of breast cancer in a patient.
CC   They can also be used to treat breast cancer. Antibodies against these
CC   polypeptides can be used to detect and monitor progression of breast
CC   cancer in patients. Primers and probes derived from the polynucleotides
CC   encoding the breast proteins are useful for detection of breast cancer.
CC   Peripheral blood cells from a patient incubated in the presence of at
CC   least one polypeptide, such that T cells proliferate, are useful in
CC   manufacture of a medicament for treating breast cancer in a patient.
CC   Antigen presenting cells incubated in the presence of at least one
CC   polypeptide are also useful for treating breast cancer.
XX
SQ   Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 other;


  Query Match           100.0%;  Score 1079;  DB 20;  Length 1079;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1079;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     181 tattaaatggcctcacatcctgaatgcaggaatgtgttcgtttaaataaacattaatctt 240
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Qy     301 tagtacattatttcctccacagcaaacctacctttccagaaggtggaaattgtatttgca 360
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Db     301 tagtacattatttcctccacagcaaacctacctttccagaaggtggaaattgtatttgca 360

Qy     361 acaatcagggcaaaacccacacttgaaaagcattttacaatattatatctaagttgcaca 420
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Db     361 acaatcagggcaaaacccacacttgaaaagcattttacaatattatatctaagttgcaca 420

Qy     421 gaagaccccagtgatcactaggaaatctaccacagtccagtttttctaatccaagaaggt 480
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Qy     481 caaacttcggggaataatgtgtccctcttctgctgctgctctgaaaaatattcgatcaaa 540
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Qy     541 acgaagtttacaagcagcagttattccaagattagagttcatttgtgtatcccatgtata 600
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Qy     601 ctggcaatgtttaggtttgcccaaaaactcccagacatccacaatgttgttgggtaaacc 660
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Qy     721 tgactctggagcctcttgcatttttctttaaaaccatttttaactgattcattcgttccgc 780
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Db     721 tgactctggagcctcttgcatttttctttaaaaccatttttaactgattcattcgttccgc 780

Qy     781 agcatgcccctctggtgctctccaaatgggatgtcataaggcaaagctcatttcctgacac 840
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Qy     841 attcacatgcacacataaaaggtttctcatcatttttggtacttggaaaaggaataatctc 900
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Qy     901 ttggctttttaatttcactcttgatttcttcaacattatagctgtgaaaatatccttcttc 960
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Qy    1021 aataacttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079
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Db    1021 aataacttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079


RESULT   2
AAC79438
ID   AAC79438 standard; cDNA; 1079 BP.
XX
AC   AAC79438;
XX
DT   07-FEB-2001  (first entry)
XX
DE   cDNA sequence of human breast tumour clone 1015D11.
XX
KW   Human; breast tumour antigen; cytostatic; immunotherapy;
KW   breast cancer; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061756-A2.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US09688.
XX
PR   06-APR-1999;   99US-0288950.
PR   02-JUL-1999;   99US-0346327.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Reed SG, Xu J, Dillon DC;
XX
DR   WPI; 2000-638568/61.
XX
PT   A novel isolated polypeptide comprising an immunogenic portion of a
PT   breast cancer protein useful in the detection and treatment of breast
PT   cancer -
XX
PS   Claim 4; Page 77; 95pp; English.
XX
CC   The present sequence was isolated from a breast tumour cDNA library. It
CC   is provided in a specification relating to compounds for immunotherapy
CC   and diagnosis of breast cancer. Breast tumour antigens and the
CC   polynucleotides that encode them may be used in the production of a
CC   pharmaceutical composition to be used in the treatment of breast cancer.
CC   Proliferated T cells and incubated antigen presenting cells are also
CC   required. The polypeptides and polynucleotides may also be used to
CC   produce a vaccine.
XX
SQ   Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 other;

  Query Match           100.0%;  Score 1079;  DB 21;  Length 1079;
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 Best Local Similarity   100.0%;  Pred. No. 0;
 Matches 1079;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 tatttcggtgcctgaatggaaaaatataaacattagctcagagacaatggggtacctgtt 120
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Qy     121 tggaatccagctggcagctataagcaccgttgaaaactctgacaggctttgtgccctttt 180
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Db     121 tggaatccagctggcagctataagcaccgttgaaaactctgacaggctttgtgccctttt 180

Qy     181 tattaaatggcctcacatcctgaatgcaggaatgtgttcgtttaaataaacattaatctt 240
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Qy     241 taatgttgaattctgaaaacacaaccataaatcatagttggttttctgtgacaatgatc 300
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Qy     721 tgactctggagcctcttgcatttttctttaaaaccatttttaactgattcattcgttccgc 780
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Db     721 tgactctggagcctcttgcatttttctttaaaaccatttttaactgattcattcgttccgc 780

Qy     781 agcatgccctctggtgctctccaaatgggatgtcataaggcaaagctcatttcctgacac 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 agcatgccctctggtgctctccaaatgggatgtcataaggcaaagctcatttcctgacac 840

Qy     841 attcacatgcacacataaaaggtttctcatcatttttggtacttggaaaaggaataatctc 900
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Db     841 attcacatgcacacataaaaggtttctcatcatttttggtacttggaaaaggaataatctc 900

Qy     901 ttggcttttttaatttcactcttgatttcttcaacattatagctgtgaaatatccttcttc 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     961 atgacctgtaataatctcataattacttgatctcttcttttaggtagctataatatggggg 1020
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Db     961 atgacctgtaataatctcataattacttgatctcttcttttaggtagctataatatggggg 1020

Qy    1021 aataacttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079
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Db    1021 aataacttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079


RESULT   3
AAI58997/c
ID   AAI58997 standard; cDNA; 1948 BP.
XX
AC   AAI58997;
XX
DT   25-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 1200.
XX
KW   human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   20-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0633450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   25-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Ormanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM39841.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 1200; 1007bpp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 other;


  Query Match           88.9%;  Score 959;  DB 22;  Length 1948;
  Best Local Similarity  99.9%;  Pred. No. 0;
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Matches 1079; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db    1281 TAATGTTGAATTCTGAAAACACAACCATAAATCATAGTTGGTTTTTCTGTGACAATGATC 1222

Qy     301 tagtacattatttcctccacagcaaacctacctttccagaaggtggaaatttgtatttgca 360
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Db    1221 TAGTACATTATTTCCTCCACAGCAAACCTACCTTTCCAGAAGGTGGAAATTTGTATTTGCA 1162

Qy     361 acaatcagggcaaaacccacacttgaaaagcattttacaatattatatctaagttgcacca 420
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Db    1161 ACAATCAGGGCAAAACCCACACTTGAAAAGCATTTTACAATATTATATCTAAGTTGCACA 1102

Qy     421 gaagaccccagtgatcactaggaaatctaccacagtccagttttctaatccaagaaggt 480
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Qy     481 -caaacttcggggaataatgtgtccctcttctgctgctgctctgaaaaatattcgatcaa 539
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Db    1041 CCAAACTTCGGGGAATAATGTGTCCCTCTTCTGCTGCTGCTCTGAAAAATATTCGATCAA 982

Qy     540 aacgaagtttacaagcagcagttattccaagattagagttcatttgtgtatcccatgtat 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981 AACGAAGTTTACAAGCAGCAGTTATTCCAAGATTAGAGTTCATTTGTGTATCCCATGTAT 922

Qy     600 actggcaatgtttaggtttgcccaaaaactcccagacatccacaatgttgtgggtaaac 659
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Db     921 ACTGGCAATGTTTAGGTTTGCCCAAAAACTCCCAGACATCCACAATGTTGTGGGTAAAC 862

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Db     861 CACCACATCTGGTAACCTCTCGATCCCTTAGATTTGTATCTCCTGCAAATATAACTGTAG 802

Qy     720 ctgactctggagcctcttgcatttttctttaaaaccatttttaactgattcattcgttccg 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     801 CTGACTCTGGAGCCTCTTGCATTTTCTTTAAAACCATTTTTAACTGATTCATTCGTTCCG 742

Qy     780 cagcatgccctctggtgctctccaaatgggatgtcataaggcaaagctcatttcctgaca 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     741 CAGCATGCCCTCTGGTGCTCTCCAAATGGGATGTCATAAGGCAAAGCTCATTTCCTGACA 682

Qy     840 cattcacatgcacacataaaaggtttctcatcattttggtacttggaaaaggaataatct 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     681 CATTCACATGCACACATAAAAGGTTTCTCATCATTTTGGTACTTGGAAAAGGAATAATCT 622

Qy     900 cttggcttttaatttcactcttgatttcttcaacattatagctgtgaaatatccttctt 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     621 CTTGGCTTTTTAATTTCACTCTTGATTTCTTCAACATTATAGCTGTGAAATATCCTTCTT 562

Qy     960 catgacctgtaataatcttcataatttacttgatcttcttctttaggtagctataatatgggg 1019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     561 CATGACCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTATAATATGGGG 502

Qy    1020 gaataacttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     501 GAATAACTTCCTGTAGAAATATCACATCTGGGCTGTACAAAGCTAAGTAGGAACACACCC 442
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Result   4
AAI60783/c
ID   AAI60783 standard; cDNA; 1958 BP.
XX
AC   AAI60783;
XX
DT   22-OCT-2001 (first entry)
XX
DE   Human polynucleotide SEQ ID NO 4772.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0633450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Yang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI   Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI   Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM41627.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 4772; 1007pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1958 BP; 613 A; 339 C; 442 G; 564 T; 0 other;
```

Query Match 88.9%; Score 959; DB 22; Length 1958;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1079; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      1 agtcccaagaactcaataatctcttatgttttcttttgaagacttattttaaatattaac 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1533 AGTCCCAAGAACTCAATAATCTCTTATGTTTTCTTTTGAAGACTTATTTTAAATATTAAC 1474

Qy     61 tatttcggtgcctgaatggaaaaatataaacattagctcagagacaatggggtacctgtt 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473 TATTTCGGTGCCTGAATGGAAAAATATAAACATTAGCTCAGAGACAATGGGGTACCTGTT 1414

Qy    121 tggaatccagctggcagctataagcaccgttgaaaactctgacaggctttgtgccctttt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413 TGGAATCCAGCTGGCAGCTATAAGCACCGTTGAAAACTCTGACAGGCTTTGTGCCCTTTT 1354

Qy    181 tattaaatggcctcacatcctgaatgcaggaatgtgttcgtttaaaataaacattaatctt 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1353 TATTAAATGGCCTCACATCCTGAATGCAGGAATGTGTTCGTTTAAATAAACATTAATCTT 1294

Qy    241 taatgttgaatttctgaaaacacaaccataaatcatagttggtttttctgtgacaatgatc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293 TAATGTTGAATTCTGAAAACACAACCATAAATCATAGTTGGTTTTTCTGTGACAATGATC 1234

Qy    301 tagtacattatttcctccacagcaaacctaccttccagaaggtggaaattgtatttgca 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 TAGTACATTATTTCCTCCACAGCAAACCTACCTTCCAGAAGGTGGAAATTGTATTTGCA 1174

Qy    361 acaatcagggcaaaacccacacttgaaaagcattttacaatattatatctaagttgcaca 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173 ACAATCAGGGCAAAACCCACACTTGAAAAGCATTTTACAATATTATATCTAAGTTGCACA 1114

Qy    421 gaagaccccagtgatcactaggaaatctaccacagtccagttttctaatccaagaaggt 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1113 GAAGACCCCAGTGATCACTAGGAAATCTACCACAGTCCAGTTTTCTAATCCAAGAAGGT 1054

Qy    481 -caaacttcggggaataatgtgtccctcttctgctgctctctgaaaaatattcgatcaa 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053 CCAAACTTCGGGGAATAATGTGTCCCTCTTCTGCTGCTGCTCTGAAAAATATTCGATCAA 994

Qy    540 aacgaagtttacaagcagcagtttattccaagattagagttcatttgtgtatcccatgtat 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993 AACGAAGTTTACAAGCAGCAGTTATTCCAAGATTAGAGTTCATTTGTGTATCCCATGTAT 934

Qy    600 actggcaatgtttaggtttgcccaaaaactcccagacatccacaatgttgttgggtaaac 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    933 ACTGGCAATGTTTAGGTTTGCCCAAAAACTCCCAGACATCCACAATGTTGTTGGGTAAAC 874

Qy    660 caccacatctggtaacctctcgatcccttagatttgtatctcctgcaaatataactgtag 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 CACCACATCTGGTAACCTCTCGATCCCTTAGATTTGTATCTCCTGCAAATATAACTGTAG 814

Qy    720 ctgactctggagcctcttgcatttttctttaaaaccatttttaactgattcattcgttccg 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 CTGACTCTGGAGCCICTTGCATTTTCTTTAAAACCATTTTTAACTGATTCATTCGTTCCG 754

Qy    780 cagcatgccctctggtgctctccaaatgggatgtcataaggcaaagctcatttcctgaca 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 CAGCATGCCCTCTGGTGCTCTCCAAATGGGATGTCATAAGGCAAAGCTCATTTCCTGACA 694

Qy    840 cattcacatgcacacatataaaggtttctcatcatttttggtacttggaaaaggaataatct 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 CATTCACATGCACACATAAAAGGTTTCTCATCATTTTGGTACTTGGAAAAGGAATAATCT 634

Qy    900 cttggctttttaatttcactcttgatttcttcaacattatagctgtgaaatatccttctt 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 CTTGGCTTTTTAATTTCACTCTTGATTTCTTCAACATTATAGCTGTGAAATATCCTTCTT 574

Qy    960 catgacctgtaataatctcataattacttgatctcttctttaggtagctataatatgggg 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    573 CATGACCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTATAATATGGGG 514

Qy   1020 gaataacttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 GAATAACTTCCTGTAGAAATATCACATCTGGGCTGTACAAAGCTAAGTAGGAACACACCC 454
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RESULT   5
AAZ47116/c
ID   AAZ47116 standard; cDNA; 1920 BP.
XX
AC   AAZ47116;
XX
DT   15-MAR-2000  (first entry)
XX
DE   Human CD40 receptor associated protein gene.
XX
KW   Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;
KW   immunosuppressive; antiinflammatory; immunosuppressive; antiallergic;
KW   human; CD40 receptor associated protein; CRAP; cytoplasmic domain;
KW   tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
KW   TNF receptor associated factor; TRAF; modulator; signalling pathway;
KW   diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
KW   arthritis; systemic lupus erythematosus; graft rejection; allergy;
KW   graft versus host disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO9955859-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-EP03025.
XX
PR   29-APR-1998;   98EP-0201392.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Pype SMC,  Remacle JEFJG,  Huylebroeck DFE;
XX
DR   WPI; 2000-062029/05.
DR   P-PSDB; AAY56019.
XX
PT   Novel proteins used to treat inflammatory diseases, NF-kappaB related
PT   diseases and for improvement of anti-tumor treatments
XX
PS   Claim 9; Page 37-39; 48pp; English.
XX
CC   This sequence represents the gene encoding human CD40 receptor
CC   associated protein (CRAP). CRAP is a functional protein capable of
CC   interacting with the cytoplasmic domain of CD40 and/or other receptors
CC   of the tumour necrosis factor (TNF) receptor superfamily such as CD30
CC   and TNF receptor I, where the protein has no homology to TNF receptor
CC   associated factor (TRAF)-proteins. The CD40 binding proteins can be
CC   used as modulators of the CD40 signalling pathway, especially to
CC   diagnose and treat TRAF-related, CD40-related, NF-kappaB related and/or
CC   Jun (kinase)-related diseases, and for the improvement of anti-tumour
CC   diseases. Diseases which may be treated include atherosclerosis,
CC   arthritis, multiple sclerosis, systemic lupus erythematosus, graft
CC   rejection, graft versus host disease, allergy, and autoimmune disease.
CC   The proteins can be used to sensitize tumour cells to anti-tumour
CC   treatments and to screen for compounds which interfere with the
CC   interaction of the proteins with other protein components of the
CC   TRAF, CD40 or NF-kappaB related pathway.
XX
SQ   Sequence 1920 BP; 599 A; 327 C; 435 G; 557 T; 2 other;
```

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  Query Match             84.2%;  Score 908;  DB 21;  Length 1920;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1078;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy      1 agtcccaagaactcaataatctcttatgttttcttttgaagacttattttaaatattaac 60
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Db   1502 AGTCCCAAGAACTCAATAATCTCTTATGTTTTCTTTTGAAGACTTATTTTAAATATTAAC 1443

Qy     61 tatttcggtgcctgaatggaaaaatataaacattagctcagagacaatggggtacctgtt 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442 TATTTCGGTGCCTGAATGGAAAAATATAAACATTAGCTCAGAGACAATGGGGTACCTGTT 1383
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Qy     121 tggaatccagctggcagctataagcaccgttgaaaactctgacaggctttgtgccctttt 180
           ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    1382 TGGAATCCAGCTGGCAGCTGTAAGCACCGTTGAAAACTCTGACAGGCTTTGTGCCCTTTT 1323

Qy     181 tattaaatggcctcacatcctgaatgcaggaatgtgttcgtttaaataaacattaatctt 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1322 TATTAAATGGCCTCACATCCTGAATGCAGGAATGTGTTCGTTTAAATAAACATTAATCTT 1263

Qy     241 taatgttgaatttctgaaaacacaaccataaatcatagttggtttttctgtgacaatgatc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1262 TAATGTTGAATTCTGAAAACACAACCATAAATCATAGTTGGTTTTTCTGTGACAATGATC 1203

Qy     301 tagtacattatttcctccacagcaaacctacctttccagaaggtggaaattgtatttgca 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1202 TAGTACATTATTTCCTCCACAGCAAACCTACCTTTCCAGAAGGTGGAAATTGTATTTGCA 1143

Qy     361 acaatcagggcaaaacccacacttgaaaagcatttacaatattatatctaagttgcaca 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1142 ACAATCAGGGCAAAACCCACACTTGAAAAGCATTTTACAATATTATATCTAAGTTGCACA 1083

Qy     421 gaagaccccagtgatcactaggaaatctaccacagtccagttttctaatccaagaaggt 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1082 GAAGACCCCAGTGATCACTAGGAAATCTACCACAGTCCAGTTTTTCTAATCCAAGAAGGT 1023

Qy     481 -caaacttcgggggaataatgtgtccctcttctgctgctgctctgaaaaaatattcgatcaa 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1022 CCAAACTTCGGGGGAATAATGTGTCCCTCTTCTGCTGCTGCTCTGAAAAAATATTCGATCAA 963

Qy     540 aacgaagtttacaagcagcagttattccaagattagagttcatttgtgtatcccatgtat 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     962 AACGAAGTTTACAAGCAGCAGTTATTCCAAGATTAGAGTTCATTTGTGTATCCCATGTAT 903

Qy     600 actggcaatgtttaggtttgcccaaaaactcccagacatccacaatgttgttgggtaaac 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     902 ACTGGCAATGTTTAGGTTTGCCCAAAAACTCCCAGACATCCACAATGTTGTTGGGTAAAC 843

Qy     660 caccacatctggtaacctctcgatccctagatttgtatctcctgcaaatataactgtag 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     842 CACCACATCTGGTAACCTCTCGATCCCTTAGATTTGTATCTCCTGCAAATATAACTGTAG 783

Qy     720 ctgactctggagcctcttgcatttcttttaaaaccatttttaactgattcattcgttccg 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     782 CTGACTCTGGAGCCTCTTGCATTTCTTTAAAACCATTTTTAACTGATTCATTCGTTCCG 723

Qy     780 cagcatgcccctctggtgctctccaaatgggatgtcataaggcaaagctcatttcctgaca 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     722 CAGCATGCCCTCTGGTGCTCTCCAAATGGGATGTCATAAGGCAAAGCTCATTTCCTGACA 663

Qy     840 cattcacatgcacacataaaaggtttctcatcattttggtacttggaaaaggaataatct 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     662 CATTCACATGCACACATAAAAGGTTTCTCATCATTTTGGTACTTGGAAAAGGAATAATCT 603

Qy     900 cttggctttttaatttcactcttgatttcttcaacattatagctgtgaaatatccttctt 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     602 CTTGGCTTTTTAATTTCACTCTTGATTTCTTCAACATTATAGCTGTGAAATATCCTTCTT 543

Qy     960 catgacctgtaataatctcataattacttgatctcttctttaggtagctataatatgggg 1019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     542 CATGACCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTATAATATGGGG 483

Qy    1020 gaataacttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     482 GAATAACTTCCTGTAGAAATATCACATCTGGGCTGTACAAAGCTAAGTAGGAACACACCC 423
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RESULT   6
AAX28153/c
ID   AAX28153 standard; DNA; 2499 BP.
XX
AC   AAX28153;
XX
DT   16-JUN-1999  (first entry)
XX
DE   Topoisomerase II binding protein 1 coding sequence.
XX
KW   Topoisomerase II binding protein; TopBP; anticancer agent; ds.
XX
OS   Homo sapiens.
XX
PN   JP11075856-A.
XX
PD   23-MAR-1999.
XX
PF   17-SEP-1997;   97JP-0251544.
XX
PR   17-SEP-1997;   97JP-0251544.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
PA   (TSUR/) TSURUO T.
XX
DR   WPI; 1999-257704/22.
DR   P-PSDB; AAY03182.
XX
PT   New Topoisomerase II- binding protein - useful as an anticancer
PT   agent
XX
PS   Disclosure; Page 18-19; 28pp; Japanese.
XX
CC   This sequence encodes the topoisomerase II binding protein (TopBP) of
CC   the invention. The TopBP protein is useful as an anticancer agent. TopBP
CC   can be used as the target molecule for anticancer agent.
XX
SQ   Sequence 2499 BP; 720 A; 505 C; 587 G; 687 T; 0 other;
```

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  Query Match           84.2%;  Score 908;  DB 20;  Length 2499;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1078;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       1 agtcccaagaactcaataatctcttatgttttcttttgaagacttattttaaatattaac 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1964 AGTCCCAAGAACTCAATAATCTCTTATGTTTTCTTTTGAAGACTTATTTTAAATATTAAC 1905

Qy      61 tatttcggtgcctgaatggaaaaatataaacattagctcagcgacaatggggtacctgtt 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1904 TATTTCGGTGCCTGAATGGAAAAATATAAACATTAGCTCAGAGACAATGGGGTACCTGTT 1845

Qy     121 tggaatccagctggcagctataagcaccgttgaaaactctgacaggctttgtgccctttt 180
           ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    1844 TGGAATCCAGCTGGCAGCTGTAAGCACCGTTGAAAACTCTGACAGGCTTTGTGCCCTTTT 1785

Qy     181 tattaaatggcctcacatcctgaatgcaggaatgtgttcgtttaaataaacattaatctt 240
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Db    1784 TATTAAATGGCCTCACATCCTGAATGCAGGAATGTGTTCGTTTAAATAAACATTAATCTT 1725

Qy     241 taatgttgaatttctgaaaacacaaccataaatcatagttggtttttctgtgacaatgatc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1724 TAATGTTGAATTCTGAAAACACAACCATAAATCATAGTTGGTTTTTCTGTGACAATGATC 1665

Qy     301 tagtacattatttcctccacagcaaacctacctttccagaaggtggaaattgtatttgca 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1664 TAGTACATTATTTCCTCCACAGCAAACCTACCTTTCCAGAAGGTGGAAATTGTATTTGCA 1605

Qy     361 acaatcagggcaaaacccacacttgaaaagcatttacaatattatatctaagttgcaca 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1604 ACAATCAGGGCAAAACCCACACTTGAAAAGCATTTTACAATATTATATCTAAGTTGCACA 1545

Qy     421 gaagaccccagtgatcactaggaaatctaccacagtccagttttctaatccaagaaggt 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1544 GAAGACCCCAGTGATCACTAGGAAATCTACCACAGTCCAGTTTTTCTAATCCAAGAAGGT 1485

Qy     481 -caaacttcgggggaataatgtgtccctcttctgctgctgctctgaaaaaatattcgatcaa 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1484 CCAAACTTCGGGGGAATAATGTGTCCCTCTTCTGCTGCTGCTCTGAAAAAATATTCGATCAA 1425
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Qy    650 ttgggtaaaccaccacatctggtaacctctcgatcccttagatttgtatctcctgcaaat 709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 TTGGGTAAACCACCACATCTGGTAACCTCTCGATCCCTTAGATTTGTATCTCCTGCAAAT 774

Qy    710 ataactgtagctgactctggagcctcttgcatttttctttaaaaccatttttaactgattc 769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 ATAACTGTAGCTGACTCTGGAGCCTCTTGCATTTTCTTTAAAACCATTTTTAACTGATTC 714

Qy    770 attcgttccgcagcatgccctctggtgctctccaaatgggatgtcataaggcaaagctca 829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713 ATTCGTTCCGCAGCATGCCCTCTGGTGCTCTCCAAATGGGATGTCATAAGGCAAAGCTCA 654

Qy    830 ttcctgacacattcacatgcacacataaaaggtttctcatcatttggtacttggaaaa 889
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    653 TTTCCTGACACGTTCACATGCACACATAAAAGGTTTCTCATCATTTTGGTACTTGGAAAA 594

Qy    890 ggaataatctcttggctttttaatttcactcttgatttcttcaacattatagctgtgaaa 949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 GGAATAATCTCTTGGCTTTTTAATTTCACTCTTGATTTCTTCAACATTATAGCTGTGAAA 534

Qy    950 tatccttcttcatgacctgtaataatctcataattacttgatctcttctttaggtagcta 1009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 TATCCTTCTTCATGACCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTA 474

Qy    1010 taatatgggggaataacttcctgtagaaatatcacatctgggctgtacaaagctaagtag 1069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     473 TAATATGGGGGAATAACTTCCTGTAGAAATATCACATCTGGGCTGTACAAAGCTAAGTAG 414

Qy    1070 ga 1071
           ||
Db     413 GA 412


RESULT   8
AAC98160/c
ID   AAC98160 standard; cDNA; 1296 BP.
XX
AC   AAC98160;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human colon cancer antigen nucleotide sequence SEQ ID NO:170.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW   immunomodulatory; muscular; gynaecological; gastrointestinal;
KW   nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW   neural disorder; immune system disorder; muscular disorder;
KW   reproductive disorder; gastrointestinal disorder; renal disorder;
KW   infectious disease; cardiovascular disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055351-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05883.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587534/55.
DR   P-PSDB; AAB53403.
XX
PT   Colon cancer associated gene sequences, referred to as colon cancer
PT   antigens, useful for the treatment, prevention, and diagnosis of colon
PT   disorders such as colon cancer -
XX
PS   Claim 1; Page 597; 2104pp; English.
XX
CC   AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC   called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC   human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC   neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC   vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC   can be used in gene therapy. The colon cancer antigen polynucleotides,
CC   proteins and antibodies to the proteins are useful for the prevention,
CC   treatment and diagnosis of colon disorders, such as colon cancer. The
CC   polynucleotides may be used in diagnostics and research, such as for
CC   chromosome identification, and as hybridisation probes. The proteins
CC   may also be used to prevent diseases such as neural disorders, immune
CC   system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, wounds, renal disorders, infectious
CC   diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC   AAB54007 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 1296 BP; 376 A; 250 C; 326 G; 333 T; 11 other;


  Query Match          46.4%;  Score 501;  DB 21;  Length 1296;
  Best Local Similarity  99.5%;  Pred. No. 1.4e-240;
  Matches  771;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps

Qy    306 cattatttcctccacagcaaacctacctttccagaaggtggaaattgtatttgcaacaat 365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CATTATTTCCTCCACAGCAAACCTACCTTTCCAGAAGGTGGAAATTGTATTTGCAACAAT 1142

Qy    366 cagggcaaaacccacacttgaaaagcattttacaatattatatctaagttgcacagaaga 425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGGCAAAACCCACACTTGAAAAGCATTTTACAATATTATATCTAAGTTGCACAGAAGA 1082

Qy    426 ccccagtgatcactaggaaatctaccacagtccagttttttctaatccaagaaggt-caaa 484
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1081 CCCCAGTGATCACTAGGAAATCTACCACAGTCCAGTTTTTCTAATCCAAGAAGGTCCAAA 1022

Qy    485 cttcgggaatatgtgtccctcttctgctgctgctctgaaaaatattcgatcaaaacga 544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CTTCGGGGAATAATGTGTCCCTCTTCTGCTGCTGCTCTGAAAAATATTCGATCAAAACGA 962

Qy    545 agtttacaagcagcagttattccaagattagagttcatttgtgtatcctatgtatactgg 604
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AGTTTACAAGCAGCAGTTATTCCAAGATTAGAGTTCATTTGTGTATCCCATGTATACTGG 902

Qy    605 caatgtttaggtttgcccaaaaactcccagacatccacaatgttgttggctaaaccacca 664
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAATGTTTAGGTTTRCCCAAAAACTCCCAGACATCCACAATGTTGTTGGCTAAACCACCA 842

Qy    665 catctggtaacctctcgatcccttagatttgtatctcctgcaaatataactgtagctgac 724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATCTGGTAACCTCTCGATCCCTTAGATTTGTATCTCCTGCAAATATAACTGTAGCTGAC 782

Qy    725 tctggagcctcttgcatttttctttaaaaccatttttaactgatttcattcgttccgcagca 784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TCTGGAGCCTCTTGCATTTTCTTTAAAACCATTTTTAACTGATTCATTCGTTCCGCAGCA 722

Qy    785 tgccctctggtgctctccaaatgggatgtcataaggcaaagctcatttctgacacattc 844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    721 TGCCCTCTGGTGCTCTCCAAATGGGATGTCATAAGGCAAAGCTCATTTCTGACACRTTC 662

Qy    845 acatgcacacataaaaggtttctcatcatttttggtacttggaaaaggaataatctcttgg 904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACATGCACACATAAAAGGTTTCTCATCATTTTGGTACTTGGAAAAGGAATAATCTCTTGG 602

Qy    905 cttttaatttcactcttgatttcttcaacattatagctgtgaaatatcctcttcatga 964
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    601 CTTTTAATTTCACTCTTGATTTCTTCAACATTATAGCTGTGAAATMTCCTTCTTCATGA 542

Qy    965 cctgtaataatctcataattacttgatctcttctttaggtagctatagatatgggggaata 1024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTATAATATGGGGGAATA 482
```

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Qy     540 aacgaagtttacaagcagcagttattccaagattagagttcatttgtgta   tatcat 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||.  |||||  
Db    1424 AACGAAGTTTACAAGCAGCAGTTATTCCAAGATTAGAGTTCATTTGTGTA.  CATG.AT 1365

Qy     600 actggcaatgtttaggtttgcccaaaaactcccagacatccacaatgttg  gggtaaac 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||.  ||||||||
Db    1364 ACTGGCAATGTTTAGGTTTGCCCAAAAACTCCCAGACATCCACAATGTTG..GGGTAAAC 1305

Qy     660 caccacatctggtaacctctcgatcccttagatttgtatctcctgcaaata aact tag 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||.  ||||  ||
Db    1304 CACCACATCTGGTAACCTCTCGATCCCTTAGATTTGTATCTCCTGCAAATA.AATTC.AT 1245

Qy     720 ctgactctggagcctcttgcatttttctttaaaaccatttttaactgattc  tcatt  g 779
           |||||||||||||||||||||||||||||||||||||||||||||||||..  ||||....|
Db    1244 CTGACTCTGGAGCCTCTTGCATTTTTCTTTAAAACCATTTTTAACTGATTCA.TCGT.TG 1185

Qy     780 cagcatgccctctggtgctctccaaatgggatgtcataaggcaaagctcat tcctgaaa 839
           ||||||||||||||||||||||||||||||||||||||||||||||||.||  ||||...|
Db    1184 CAGCATGCCCTCTGGTGCTCTCCAAATGGGATGTCATAAGGCAAAGCTCATTTCCTCACA 1125

Qy     840 cattcacatgcacacataaaaggtttctcatcatttttggtacttggaaaag aataa  t 899
           |||||||||||||||||||||||||||||||||||||||||||||||||||. |||||  .
Db    1124 CATTCACATGCACACATAAAAGGTTTCTCATCATTTTTGGTACTTGGAAAAGTAATAA.TT 1065

Qy     900 cttggctttttaatttcactcttgatttcttcaacattatagctgtgaaat tc tt tt 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||.  ....   |
Db    1064 CTTGGCTTTTTAATTTCACTCTTGATTTCTTCAACATTATAGCTGTGAAATATCCTTTTT 1005

Qy     960 catgacctgtaataatctcataattacttgatctcttctttaggtatctat ..tat  g 1019
           |||||||||||||||||||||||||||||||||||||||||||||||||.   ||||   |
Db    1004 CATGACCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTATTATATCGGG 945

Qy    1020 gaataacttcctgtagaaatatcacatctgggctgtacaaagctaagtag aacaca  c 1079
           |||||||||||||||||||||||||||||||||||||||||||||||.|||   .|||. ||
Db     944 GAATAATTTCCTGTAGAAATATCACATCTGGGCTGTACAAAGCTAAGTAGTAACACATCC 885
```

RESULT 7
AAH15146/c
ID AAH15146 standard; cDNA; 1898 BP.
XX
AC AAH15146;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:13209.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, [illegible] I;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Ota [illegible] ;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 13209; 2537pp - CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 1898 BP; 590 A; 327 C; 426 G; 555 T; 0 other;

```
  Query Match             74.1%;  Score 799;  DB 22;  Length 1898;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1019;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy      51 aaatattaactatttcggtgcctgaatggaaaaatataaacattagctcagagacaatgg 110
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1433 AAATATTAACTATTTCGGTGCCTGAATGGAAAAATATAAACATTAGCTCAGAGACAATGT 1374

Qy     111 ggtacctgtttggaatccagctggcagctataagcaccgttgaaaactctgacaggcttt 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1373 GGTACCTGTTTGGAATCCAGCTGGCAGCTATAAGCACCGTTGAAAACTCTGACAGGCTTT 1314

Qy     171 gtgccctttttattaaatggcctcacatcctgaatgcaggaatgtgttcgtttaaataaa 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 GTGCCCTTTTTATTAAATGGCCTCACATCCTGAATGCAGGAATGTGTTCGTTTAAATAAA 1254

Qy     231 cattaatctttaatgttgaattctgaaaacacaaccataaatcatagttggtttttctgt 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1253 CATTAATCTTTAATGTTGAATTCTGAAAACACAACCATAAATCATAGTTGGTTTTTCTGT 1194

Qy     291 gacaatgatctagtacattatttcctccacagcaaacctacctttccagaaggtggaaat 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1193 GACAATGATCTAGTACATTATTTCCTCCACAGCAAACCTACCTTTCCAGAAGGTGGAAAT 1134

Qy     351 tgtatttgcaacaatcagggcaaaacccacacttgaaaagcatttacaatattatatct 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1133 TGTATTTGCAACAATCAGGGCAAAACCCACACTTGAAAAGCATTTACAATATTATATCT 1074

Qy     411 aagttgcacagaagaccccagtgatcactaggaaatctaccacagtccagtttttctaat 470
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1073 AAGTTGCACAGAAGACCCCAGTGATCACTAGGAAATCTACCACAGTCCAGTTTTTCTAAT 1014

Qy     471 ccaagaaggt-caaacttcggggaataatgtgtccctcttctgctgctgctctgaaaaat 529
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 CCAAGAAGGTCCAAACTTCGGGGAATAATGTGTCCCTCTTCTGCTGCTGCTCTGAAAAAT 954

Qy     530 attcgatcaaaacgaagtttacaagcagcagttattccaagattagagttcatttgtgta 589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     953 ATTCGATCAAAACGAAGTTTACAAGCAGCAGTTATTCCAAGATTAGAGTTCATTTGTGTA 894

Qy     590 tcccatgtatactggcaatgtttaggtttgcccaaaaactcccagacatccacaatgttg 649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     893 TCCCATGTATACTGGCAATGTTTAGGTTTGCCCAAAAACTCCCAGACATCCACAATGTTG 834
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Qy    1025 acttcctgtagaaatatcacatctgggctgtacaaagctaagtaggaacacaccc 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ACTTCCTGTAGAAATATCACATCTGGGCTGTACAAAGCTAAGTAGGAACACACCC 427


RESULT  9
AAH08073/c
ID   AAH08073 standard; cDNA; 752 BP.
XX
AC   AAH08073;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:4908.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 1; SEQ ID 4908; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 752 BP; 225 A; 148 C; 200 G; 176 T; 3 other;

  Query Match           19.4%;  Score 209;  DB 22;  Length 752;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-94;
  Matches  209;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     863 tttctcatcattttggtacttggaaaaggaataatctcttggctttttaatttcactctt 922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     620 TTTCTCATCATTTTGGTACTTGGAAAAGGAATAATCTCTTGGCTTTTTAATTTCACTCTT 561

Qy     923 gatttcttcaacattatagctgtgaaatatccttcttcatgacctgtaataatctcataa 982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     560 GATTTCTTCAACATTATAGCTGTGAAATATCCTTCTTCATGACCTGTAATAATCTCATAA 501

Qy     983 ttacttgatctcttctttaggtagctataatatgggggaataacttcctgtagaaatatc 1042
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     500 TTACTTGATCTCTTCTTTAGGTAGCTATAATATGGGGGAATAACTTCCTGTAGAAATATC 441

Qy    1043 acatctgggctgtacaaagctaagtagga 1071
           |||||||||||||||||||||||||||||
Db     440 ACATCTGGGCTGTACAAAGCTAAGTAGGA 412


RESULT  10
AAI15311/c
ID   AAI15311 standard; DNA; 444 BP.
XX
AC   AAI15311;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #5244 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 25; SEQ ID No 5244; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging
CC   of diseases of the cervix, notably cervical cancer.
CC   Note: The sequence data for this patent did not form part of the print
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 444 BP; 138 A; 60 C; 80 G; 166 T; 0 other;
```

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  Query Match             8.7%;  Score 94;  DB 22;  Length 444;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-37;
  Matches   94;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     964 acctgtaataatctcataattacttgatctcttctttaggtagctataatatgggggaat 1023
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     346 ACCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTATAATATGGGGGAAT 287

Qy    1024 aacttcctgtagaaatatcacatctgggctgtac 1057
           ||||||||||||||||||||||||||||||||||
Db     286 AACTTCCTGTAGAAATATCACATCTGGGCTGTAC 253


RESULT  11
AAI24484/c
ID   AAI24484 standard; DNA; 691 BP.
XX
AC   AAI24484;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #14417 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 25; SEQ ID No 14417; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging
CC   of diseases of the cervix, notably cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 691 BP; 230 A; 81 C; 112 G; 268 T; 0 other;


  Query Match             8.7%;  Score 94;  DB 22;  Length 691;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-37;
  Matches   94;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     964 acctgtaataatctcataattacttgatctcttctttaggtagctataatatgggggaat 1023
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 ACCTGTAATAATCTCATAATTACTTGATCTCTTCTTTAGGTAGCTATAATATGGGGGAAT 149

Qy    1024 aacttcctgtagaaatatcacatctgggctgtac 1057
           ||||||||||||||||||||||||||||||||||
Db     148 AACTTCCTGTAGAAATATCACATCTGGGCTGTAC 115


RESULT  12
AAX40590/c
ID   AAX40590 standard; cDNA; 483 BP.
XX
AC   AAX40590;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Human secreted protein 5' EST SEQ ID No: 190.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906550-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB01232.
XX
PR   01-AUG-1997;   97US-0905144.
XX
PA   (GEST ) GENSET.
XX
PI   Duclert A,  Dumas Milne Edwards J,  Lacroix B;
XX
DR   WPI; 1999-153780/13.
DR   P-PSDB; AAY11868.
XX
PT   New isolated prostate-derived nucleic acids - used to develop
PT   products which may have cytokine, immune regulatory, haematopoiesis
PT   regulating, anti-inflammatory or tumour inhibition activity
XX
PS   Claim 1; Page 298; 675pp; English.
XX
CC   AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins expressed in prostate, and encode the proteins
CC   given in AAY11716 to AAY11993 respectively. The proteins given represent
CC   the signal peptide and an N-terminal fragment of a secreted protein. The
CC   nucleic acid sequences can be used for producing secreted human gene
CC   products. They can also be used to develop products for diagnosis and
CC   therapy. The proteins obtained may have cytokine activity, cell
CC   proliferation and differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptides can be used f.:
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ   Sequence 483 BP; 123 A; 111 C; 139 G; 110 T; 0 other;


  Query Match             7.4%;  Score 80;  DB 20;  Length 483;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-30;
  Matches   80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy   1000 taggtagctataatatgggggaataacttcctgtagaaatatcacatctgggctgtacaa 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 TAGGTAGCTATAATATGGGGGAATAACTTCCTGTAGAAATATCACATCTGGGCTGTACAA 424

Qy   1060 agctaagtaggaacacaccc 1079
          ||||||||||||||||||||
Db    423 AGCTAAGTAGGAACACACCC 404


RESULT  13
AAZ68598
ID   AAZ68598 standard; DNA; 47 BP.
XX
AC   AAZ68598;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:2947.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,C)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;    99WO-IB00822.
XX
PR   21-APR-1998;    98US-0082614.
PR   23-NOV-1998;    98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome -
XX
PS   Claim 3; Page 859; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 11 A; 6 C; 6 G; 24 T; 0 other;


  Query Match             4.4%;  Score 47;  DB 21;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-13;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     27 tgttttcttttgaagacttatttaaatattaactatttcggtgcct 73
          |||||||||||||||||||||||||||||||||||||||||||||
Db      1 tgttttcttttgaagacttatttaaatattaactatttcggtgcct 47


RESULT  14
AAH13035
ID   AAH13035 standard; cDNA; 579 BP.
XX
AC   AAH13035;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA clone (3'-primer) SEQ ID NO:9870.
XX
KW   Human; primer; detection; diagnosis; antisense therapy, gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 3; SEQ ID 9870; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 579 BP; 204 A; 97 C; 79 G; 191 T; 8 other;
```

```
  Query Match             4.2%;  Score 45;  DB 22;  Length 579;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 aaatattaactatttcggtgcctgaatggaaaaatataaacatta 95
           |||||||||||||||||||||||||||||||||||||||||||||
Db     467 aaatattaactatttcggtgcctgaatggaaaaatataaacatta 511


RESULT  15
AAZ47119/c
ID   AAZ47119 standard; cDNA; 1312 BP.
XX
AC   AAZ47119;
XX
DT   15-MAR-2000  (first entry)
XX
DE   Mouse CD40 receptor associated protein gene.
XX
KW   Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;
KW   immunosuppressive; antiinflammatory; immunosuppressive; antiallergic;
KW   mouse; CD40 receptor associated protein; CRAP; cytoplasmic domain;
KW   tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
KW   TNF receptor associated factor; TRAF; modulator; signalling pathway;
KW   diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
KW   arthritis; systemic lupus erythematosus; graft rejection; allergy;
KW   graft versus host disease; autoimmune disease; ds.
XX
OS   Mus musculus.
XX
PN   WO9955859-A2.
XX
PD   04-NOV-1999.
XX
PF   28-APR-1999;   99WO-EP03025.
XX
PR   29-APR-1998;   98EP-0201392.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Pype SMC,  Remacle JEFJG,  Huylebroeck DFE;
XX
DR   WPI; 2000-062029/05.
DR   P-PSDB; AAY56020.
XX
PT   Novel proteins used to treat inflammatory diseases, NF-kappaB related
PT   diseases and for improvement of anti-tumor treatments -
XX
PS   Claim 10; Page 41-43; 48pp; English.
XX
CC   This sequence represents the gene encoding mouse CD40 receptor
CC   associated protein (CRAP). CRAP is a functional protein capable of
CC   interacting with the cytoplasmic domain of CD40 and/or other receptors
CC   of the tumour necrosis factor (TNF) receptor superfamily such as CD30
CC   and TNF receptor I, where the protein has no homology to TNF receptor
CC   associated factor (TRAF)-proteins. The CD40 binding proteins can be
CC   used as modulators of the CD40 signalling pathway, especially to
CC   diagnose and treat TRAF-related, CD40-related, NF-kappaB related and/or
CC   Jun (kinase)-related diseases, and for the improvement of anti-tumour
CC   diseases. Diseases which may be treated include atherosclerosis,
CC   arthritis, multiple sclerosis, systemic lupus erythematosus, graft
CC   rejection, graft versus host disease, allergy, and autoimmune disease.
CC   The proteins can be used to sensitize tumour cells to anti-tumour
CC   treatments and to screen for compounds which interfere with the
CC   interaction of the proteins with other protein components of the
CC   TRAF, CD40 or NF-kappaB related pathway.
XX
SQ   Sequence 1312 BP; 359 A; 279 C; 352 G; 322 T; 0 other;


  Query Match             3.3%;  Score 36;  DB 21;  Length 1312;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   36;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     789 ctctggtgctctccaaatgggatgtcataaggcaaa 824
           ||||||||||||||||||||||||||||||||||||
Db     845 CTCTGGTGCTCTCCAAATGGGATGTCATAAGGCAAA 810


RESULT  16
AAH33140
ID   AAH33140 standard; cDNA; 417 BP.
XX
AC   AAH33140;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:196.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome X; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US26524.
XX
PR   29-SEP-1999;   99US-0157137.
PR   03-NOV-1999;   99US-0163280.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG73709.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS   Claim 1; Page 2344; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where
CC   the proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene
CC   therapy and vaccine production. N and P may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate P
CC   expression. For example, N and P may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P by expressing
CC   inactive proteins or to supplement the patients own production of P.
CC   Additionally, N may be used to produce the colon cancer-associated Ps,
CC   by inserting the nucleic acids into a host cell and culturing the cell
CC   to express the proteins. N and P can be used in the prevention, diagnosis
CC   and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC   and AAB77789 represent sequences used in the exemplification of the
CC   present invention.
CC   N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC   missing at time of publication, meaning no sequences are present for
CC   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence 417 BP; 118 A; 61 C; 65 G; 172 T; 1 other;


  Query Match             1.9%;  Score 21;  DB 22;  Length 417;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     459 agttttctaatccaagaagg 479
           |||||||||||||||||||||
Db     149 agttttctaatccaagaagg 169
```

```
RESULT 17
AAV55038
ID   AAV55038 standard; cDNA; 5232 BP.
XX
AC   AAV55038;
XX
DT   13-NOV-1998 (first entry)
XX
DE   Human XIAP coding sequence.
XX
KW   Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW   proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             34..1527
FT                   /*tag= a
FT                   /product= XIAP
XX
PN   WO9835693-A2.
XX
PD   20-AUG-1998.
XX
PF   13-FEB-1998;   98WO-IB00781.
XX
PR   13-FEB-1997;   97US-0800929.
XX
PA   (UYOT-) UNIV OTTAWA.
XX
PI   Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI   Tsang B;
XX
DR   WPI; 1998-467164/40.
DR   P-PSDB; AAW69294.
XX
PT   Inducing apoptosis in proliferative mammalian cells with inhibitor
PT   of IAP or NAIP polypeptide - also methods for prognosis based on
PT   presence of IAP and NAIP, specifically applied to cancers involving
PT   p53 mutations
XX
PS   Claim 13; Fig 1; 147pp; English.
XX
CC   This sequence encodes the human XIAP protein, which is a inhibitor of
CC   apoptosis protein (IAP), and can be used in the method of the invention.
CC   The method is for enhancing apoptosis in cells from a mammal with
CC   proliferative disease by treatment with a compound that inhibits
CC   biological activity of an IAP or NAIP polypeptide. The inhibitory
CC   compounds are used to treat proliferative diseases, specially cancers of
CC   ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC   liver nasopharnyx, thyroid,central nervous system, prostate, colon,
CC   rectum, cervix or endometrium, particularly to increase their sensitivity
CC   to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC   detected in many cancers and are associated with poor prognosis,
CC   resistance to chemotherapeutic agents and mutations in p53 (it is
CC   suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC   genes). Transgenic animals are used for testing the effects of antisense
CC   oligonucleotides and for screening for the inhibitors.
XX
SQ   Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;

  Query Match             1.9%;  Score 21;  DB 19;  Length 5232;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     459 agtttttctaatccaagaagg 479
           |||||||||||||||||||||
Db    2498 agtttttctaatccaagaagg 2518


RESULT 18
AAC31359
ID   AAC31359 standard; cDNA; 237 BP.
XX
AC   AAC31359;
XX
DT   06-OCT-2000 (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 35434.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 35434; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 237 BP; 59 A; 72 C; 65 G; 37 T; 4 other;

  Query Match             1.9%;  Score 20;  DB 21;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     417 cacagaagaccccagtgatc 436
           ||||||||||||||||||||
Db     125 cacagaagaccccagtgatc 144


RESULT 19
AAC34438/c
ID   AAC34438 standard; DNA; 577 BP.
XX
AC   AAC34438;
XX
DT   17-OCT-2000 (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 6656.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
```

KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
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Query Match 1.9%; Score 20; DB 21; Length 577;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    912 atttcactcttgatttcttc 931
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Db    224 ATTTCACTCTTGATTTCTTC 205
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RESULT 20
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ID AAC44257 standard; DNA; 960 BP.
XX
AC AAC44257;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 42196.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 29-OCT-1999; 99US-0162142.

Query Match 1.9%; Score 20; DB 21; Length 960;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 912 atttcactcttgatttcttc 931
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Db 224 ATTTCACTCTTGATTTCTTC 205

RESULT 21
AAZ76456/c
ID AAZ76456 standard; DNA; 19 BP.
XX
AC AAZ76456;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:10812.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
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PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.

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PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome -
XX
PS   Claim 9; Page 2535; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 19 BP; 7 A; 5 C; 2 G; 5 T; 0 other;


  Query Match             1.8%;  Score 19;  DB 21;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     207 caggaatgtgttcgtttaa 225
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Db      19 CAGGAATGTGTTCGTTTAA 1


RESULT  22
AAH69026
ID   AAH69026 standard; cDNA; 338 BP.
XX
AC   AAH69026;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human cervical cancer marker nucleic acid 300.
XX
KW   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142467-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33312.
XX
PR   08-DEC-1999;   99US-0169681.
PR   21-DEC-1999;   99US-0171350.
PR   14-MAR-2000; 2000US-0189315.
PR   12-MAY-2000; 2000US-0203791.
PR   09-JUN-2000; 2000US-0210600.
PR   21-JUL-2000; 2000US-0220114.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Deeds J,  Berger A,  Zhao X;
XX
DR   WPI; 2001-375006/39.
XX
PT   New isolated nucleic acid for diagnosing and treating cervical cancer
PT   and for assessing and detecting compounds for treating the cancer -
XX
PS   Claim 1; Page 156; 1051pp; English.
XX
CC   The invention relates to novel genes (AAH68727-AAH73383) associated with
CC   cervical cancer with cytostatic activity. The nucleic acids and encoded
CC   polypeptides are useful: to assess if a patient is afflicted with
CC   cervical cancer or has a pre-malignant condition; to monitor the
CC   progression of cervical cancer or a premalignant condition in a patient;
CC   and to select and/or assess the efficacy of a compound or therapy for
CC   inhibiting cervical cancer in a patient. The nucleic acids may also be
CC   useful for gene therapy.
XX
SQ   Sequence 338 BP; 89 A; 79 C; 73 G; 97 T; 0 other;


  Query Match             1.8%;  Score 19;  DB 22;  Length 338;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     319 acagcaaacctacctttcc 337
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Db     218 acagcaaacctacctttcc 236


RESULT  23
AAH71896
ID   AAH71896 standard; cDNA; 351 BP.
XX
AC   AAH71896;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human cervical cancer marker nucleic acid 3170.
XX
KW   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142467-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33312.
XX
PR   08-DEC-1999;   99US-0169681.
PR   21-DEC-1999;   99US-0171350.
PR   14-MAR-2000; 2000US-0189315.
PR   12-MAY-2000; 2000US-0203791.
PR   09-JUN-2000; 2000US-0210600.
PR   21-JUL-2000; 2000US-0220114.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Deeds J,  Berger A,  Zhao X;
XX
DR   WPI; 2001-375006/39.
XX
PT   New isolated nucleic acid for diagnosing and treating cervical cancer
PT   and for assessing and detecting compounds for treating the cancer -
XX
PS   Claim 1; Page 626; 1051pp; English.
XX
CC   The invention relates to novel genes (AAH68727-AAH73383) associated with
CC   cervical cancer with cytostatic activity. The nucleic acids and encoded
CC   polypeptides are useful: to assess if a patient is afflicted with
CC   cervical cancer or has a pre-malignant condition; to monitor the
CC   progression of cervical cancer or a premalignant condition in a patient;
CC   and to select and/or assess the efficacy of a compound or therapy for
CC   inhibiting cervical cancer in a patient. The nucleic acids may also be
CC   useful for gene therapy.
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XX
SQ   Sequence 351 BP; 98 A; 78 C; 73 G; 102 T; 0 other;


  Query Match             1.8%;  Score 19;  DB 22;  Length 351;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     319 acagcaaacctacctttcc 337
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Db     208 acagcaaacctacctttcc 226


RESULT  24
AAH70689
ID   AAH70689 standard; cDNA; 494 BP.
XX
AC   AAH70689;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human cervical cancer marker nucleic acid 1963.
XX
KW   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142467-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33312.
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PR   08-DEC-1999;   99US-0169681.
PR   21-DEC-1999;   99US-0171350.
PR   14-MAR-2000; 2000US-0189315.
PR   12-MAY-2000; 2000US-0203791.
PR   09-JUN-2000; 2000US-0210600.
PR   21-JUL-2000; 2000US-0220114.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Deeds J,  Berger A,  Zhao X;
XX
DR   WPI; 2001-375006/39.
XX
PT   New isolated nucleic acid for diagnosing and treating cervical cancer
PT   and for assessing and detecting compounds for treating the cancer -
XX
PS   Claim 1; Page 420-421; 1051pp; English.
XX
CC   The invention relates to novel genes (AAH68727-AAH73383) associated with
CC   cervical cancer with cytostatic activity. The nucleic acids and encoded
CC   polypeptides are useful: to assess if a patient is afflicted with
CC   cervical cancer or has a pre-malignant condition; to monitor the
CC   progression of cervical cancer or a premalignant condition in a patient;
CC   and to select and/or assess the efficacy of a compound or therapy for
CC   inhibiting cervical cancer in a patient. The nucleic acids may also be
CC   useful for gene therapy.
XX
SQ   Sequence 494 BP; 128 A; 106 C; 114 G; 146 T; 0 other;


  Query Match             1.8%;  Score 19;  DB 22;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     319 acagcaaacctacctttcc 337
           ||||||||||||||||||||
Db     220 acagcaaacctacctttcc 238


RESULT  25
AAH72662/c
ID   AAH72662 standard; cDNA; 494 BP.
XX
AC   AAH72662;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human cervical cancer marker nucleic acid 3936.
XX
KW   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142467-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33312.
XX
PR   08-DEC-1999;   99US-0169681.
PR   21-DEC-1999;   99US-0171350.
PR   14-MAR-2000; 2000US-0189315.
PR   12-MAY-2000; 2000US-0203791.
PR   09-JUN-2000; 2000US-0210600.
PR   21-JUL-2000; 2000US-0220114.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Deeds J,  Berger A,  Zhao X;
XX
DR   WPI; 2001-375006/39.
XX
PT   New isolated nucleic acid for diagnosing and treating cervical cancer
PT   and for assessing and detecting compounds for treating the cancer -
XX
PS   Claim 1; Page 787; 1051pp; English.
XX
CC   The invention relates to novel genes (AAH68727-AAH73383) associated with
CC   cervical cancer with cytostatic activity. The nucleic acids and encoded
CC   polypeptides are useful: to assess if a patient is afflicted with
CC   cervical cancer or has a pre-malignant condition; to monitor the
CC   progression of cervical cancer or a premalignant condition in a patient;
CC   and to select and/or assess the efficacy of a compound or therapy for
CC   inhibiting cervical cancer in a patient. The nucleic acids may also be
CC   useful for gene therapy.
XX
SQ   Sequence 494 BP; 147 A; 101 C; 101 G; 143 T; 2 other;


  Query Match             1.8%;  Score 19;  DB 22;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     319 acagcaaacctacctttcc 337
           ||||||||||||||||||||
Db     249 ACAGCAAACCTACCTTTCC 231


RESULT  26
AAX22252
ID   AAX22252 standard; DNA; 861 BP.
XX
AC   AAX22252;
XX
DT   18-MAY-1999  (first entry)
XX
DE   Human secreted protein gene 42 clone HSNAD72.
XX
KW   Human; secreted protein; gene therapy; protein therapy; cancer; weight;
KW   tumour; chromosome mapping; forensic; haematological disease; allergy;
KW   inflammation; cell proliferation; viral infection; wound healing;
KW   modulation; appetite; behaviour; food additive; preservative; ss.
XX
```

OS Homo sapiens.
XX
PN WO9903990-A1.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US14613.
XX
PR 18-AUG-1997; 97US-0056361.
PR 16-JUL-1997; 97US-0052661.
PR 16-JUL-1997; 97US-0052870.
PR 16-JUL-1997; 97US-0052871.
PR 16-JUL-1997; 97US-0052872.
PR 16-JUL-1997; 97US-0052873.
PR 16-JUL-1997; 97US-0052874.
PR 16-JUL-1997; 97US-0052875.
PR 22-JUL-1997; 97US-0053440.
PR 22-JUL-1997; 97US-0053441.
PR 22-JUL-1997; 97US-0053442.
PR 18-AUG-1997; 97US-0055683.
PR 18-AUG-1997; 97US-0055724.
PR 18-AUG-1997; 97US-0055725.
PR 18-AUG-1997; 97US-0055726.
PR 18-AUG-1997; 97US-0055946.
PR 18-AUG-1997; 97US-0055952.
PR 18-AUG-1997; 97US-0055985.
PR 18-AUG-1997; 97US-0055989.
PR 18-AUG-1997; 97US-0056359.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Duan R, Feng P, Ferrie AM, Florence KA, Fouad J;
PI Greene JM, Hu J, Ni J, Rosen CA, Ruben SM, Young PE;
PI Yu G;
XX
DR WPI; 1999-132234/11.
DR P-PSDB; AAY01424.
XX
PT New nucleic acids encoding secreted human proteins - potentially
PT useful for treating and diagnosing diseases and identifying specific
PT binding agents
XX
PS Claim 4; Page 190-191; 251pp; English.
XX
CC The invention relates to nucleic acid sequences (AAX22211 to AAX22282)
CC encoding human secreted proteins (AAY01383 to AAY01454). The secreted
CC protein gene sequences are deposited with the ATCC under deposit number
CC ATCC 209138, 209139 or 209141. Host cells containing vectors comprising
CC the nucleic acid sequences are used for the recombinant expression of
CC the secreted proteins. The polynucleotide and amino acid sequences are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also diagnosed
CC by determining the amount of the new polypeptides in a sample or by the
CC presence of mutations in the new polynucleotides. The nucleic acid
CC sequences, or its fragments, are useful for chromosome identification
CC and mapping; as antisense and triplex-forming therapeutics; in gene
CC therapy; for (forensic) identification of individuals; as molecular
CC weight markers; to identify related sequences or specific mRNA; in
CC preparation of oligomers and to raise anti-DNA antibodies. Antibodies are
CC useful as immunoassay reagents (including for in vivo imaging) and
CC therapeutically to inhibit or activate particular polypeptides. A very
CC wide range of disorders may be treated with the polynucleotide and
CC polypeptide sequences, e.g. autoimmune or haematological diseases,
CC allergy, inflammation, cancer or other forms of cell proliferation, viral
CC or other infections. The sequences may also be useful in wound healing,
CC to modulate differentiation of embryonic stem cells, to modulate weight,
CC appetite, behaviour etc. and as food additive or preservative. The
CC present sequence represents a gene encoding a human secreted protein
CC (see descriptor line for gene number and clone identification).
XX
SQ Sequence 861 BP; 222 A; 226 C; 164 G; 245 T; 4 other;

Query Match 1.8%; Score 19; DB 20; Length 861;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 agcctcttgcatttttctt 748
||||||||||||||||||||
Db 357 agcctcttgcatttttctt 375

RESULT 27
AAN71405
ID AAN71405 standard; DNA; 1864 BP.
XX
AC AAN71405;
XX
DT 18-APR-1991 (first entry)
XX
DE Sequence of ANS-1 which increases transformation efficiency.
XX
KW Enzyme; fungal expression vector; Aspergillus expression vector;
KW Trichoderma; ds.
XX
OS Mucor miehei.
XX
PN EP215594-A.
XX
PD 25-MAR-1987.
XX
PF 27-AUG-1986; 86EP-0306624.
XX
PR 07-JUL-1986; 86US-0882224.
PR 29-AUG-1985; 85US-0771374.
XX
PA (GENE-) GENENCOR INC.
XX
PI Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
XX
DR WPI; 1987-095049/14.
XX
PT New DNA sequences for expressing polypeptide in filamentous fungi
PT - with secretion of prod. from the cells, and new vectors and
PT transformed fungi
XX
PS Example; Fig 13; 45pp; English.
XX
CC A DNA sequence coding for a heterologous polypeptide which can be
CC expressed in and secreted from filamentous fungi is claimed. Pref.
CC the DNA sequence codes for bovine preprochymosin, M. meihei
CC preprocarboxyl protease or A. niger preproglucoamylase. Also new
CC are vectors consisting of the DNA sequence plus an operably-linked
CC signal sequence. The vectors may also include a sequence which
CC increases transformation efficiency, e.g. ANS-1.
XX
SQ Sequence 1864 BP; 786 A; 210 C; 44 G; 732 T; 92 other;

Query Match 1.8%; Score 19; DB 8; Length 1864;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 ttattttaaatattaacta 62
||||||||||||||||||||
Db 1161 ttattttaaatattaacta 1179

RESULT 28
AAQ78892
ID AAQ78892 standard; DNA; 1864 BP.
XX
AC AAQ78892;
XX
DT 17-DEC-1995 (first entry)
XX

DE Aspergillus nidulans ANS-1 partial sequence.
XX
KW Vector; transformation; protein secretion; ds.
XX
OS Aspergillus nidulans.
XX
PN EP625577-A1.
XX
PD 23-NOV-1994.
XX
PF 27-AUG-1986; 86EP-0201751.
XX
PR 29-AUG-1985; 85US-0771374.
PR 07-JUL-1986; 86US-0882224.
XX
PA (GEMV) GENENCOR INT INC.
XX
PI Berka RM, Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
XX
DR WPI; 1994-359750/45.
XX
PT Vectors and DNA for expressing polypeptide(s) in filamentous fungi
PT - include secretory signal sequences that are native or foreign to
PT heterologous polypeptide(s), such as chymosin or glucoamylase.
XX
PS Disclosure; Fig 13A-13B; 50pp; English.
XX
CC The sequence represents the A. nidulans ANS-1 sequence which is
CC included in the construction of transformation vectors for
CC recombinant protein expression and secretion from a filamentous
CC fungus host. The sequence increases the transformation efficiency
CC of the vector. This illustrates the main claims of the patent,
CC which provide a vector containing (i) DNA encoding a heterologous
CC polypeptide (chymosin, prochymosin, preprochymosin, Aspergillus
CC niger glucoamylase, Humicola grisea glucoamylase or M. miehei
CC carboxyl protease) and (ii) a secretory signal peptide, and a
CC filamentous fungus (Aspergillus, Trichoderma, Neurospora,
CC Podospora, Endothia, Mucor, Cochiobolus or Pyriclaria, especially A.
CC nidulans, A. awamori or T. reesei) transformed with the vector for
CC recombinant protein (enzyme) production.
XX
SQ Sequence 1864 BP; 819 A; 193 C; 120 G; 732 T; 0 other;

Query Match 1.8%; Score 19; DB 15; Length 1864;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 ttatttaaatattaacta 62
||||||||||||||||||
Db 1161 ttatttaaatattaacta 1179

RESULT 29
AAF92529/c
ID AAF92529 standard; DNA; 2438 BP.
XX
AC AAF92529;
XX
DT 16-MAY-2001 (first entry)
XX
DE Rat T2R02 nucleotide sequence SEQ ID NO:80.
XX
KW Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor;
KW taste transduction G-protein coupled receptor; identification; tongue;
KW taste sensory neuron; taste cell; taste modulator; food;
KW taste signalling pathway; ds.
XX
OS Rattus sp.
XX
PN WO200118050-A2.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US24821.
XX
PR 10-SEP-1999; 99US-0393634.
PR 22-FEB-2000; 2000US-0510332.
XX
PA (REGC) UNIV CALIFORNIA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Zuker CS, Adler JE, Ryba N, Mueller K, Hoon M;
XX
DR WPI; 2001-211396/21.
DR P-PSDB; AAB87782.
XX
PT Nucleic acids encoding the T2R family of G-protein coupled taste
PT receptors, useful for identifying taste modulators that can be used in
PT food and pharmaceutical industries to customize taste, for e.g. to
PT decrease the bitter taste of food -
XX
PS Claim 51; Page 190-191; 249pp; English.
XX
CC AAF92502 to AAF92572 represent nucleic acids which encode taste
CC transduction G-protein coupled receptors designated T2R proteins.
CC AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
CC represent T2R family consensus sequences from the present invention.
CC The T2R proteins are taste modulators. The nucleic acids are useful as
CC probes for the identification of taste cells, as the nucleic acids are
CC specifically expressed in taste cells. They also serve as tools for the
CC generation of taste topographic maps that elucidate the relationship
CC between the taste cells of the tongue and taste sensory neurons leading
CC to taste centres in the brain. The taste modulators are useful for
CC pharmacological and genetic modulation of taste signalling pathways.
CC Modulatory compounds comprising T2R proteins can therefore be used in
CC food and pharmaceutical industries to customise taste, for e.g. to
CC decrease the bitter taste of food or drugs.
XX
SQ Sequence 2438 BP; 714 A; 459 C; 470 G; 795 T; 0 other;

Query Match 1.8%; Score 19; DB 22; Length 2438;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 899 tcttggctttttaatttca 917
||||||||||||||||||
Db 215 TCTTGGCTTTTTAATTTCA 197

RESULT 30
AAI59313/c
ID AAI59313 standard; cDNA; 2706 BP.
XX
AC AAI59313;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1516.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX

PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM40157.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 1516; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 2706 BP; 788 A; 559 C; 604 G; 755 T; 0 other;

Query Match 1.8%; Score 19; DB 22; Length 2706;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 gagcctcttgcattttctt 747
||||||||||||||||||
Db 1614 GAGCCTCTTGCATTTTCTT 1596

RESULT 31
AAX13252/c
ID AAX13252 standard; DNA; 4605 BP.
XX
AC AAX13252;
XX
DT 19-MAR-1999 (first entry)
XX
DE Enterococcus faecalis genome contig SEQ ID NO:315.
XX
KW Enterococcus faecalis; contig; detection; Enterococcal infection;
KW vaccine; attenuation; computer readable medium; ds.
XX
OS Enterococcus faecalis.
XX
PN WO9850555-A2.
XX
PD 12-NOV-1998.
XX
PF 04-MAY-1998; 98WO-US08985.
XX
PR 14-NOV-1997; 97US-0066009.
PR 06-MAY-1997; 97US-0044031.
PR 16-MAY-1997; 97US-0046655.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Barash SC, Dillon PJ, Kunsch CA;
XX
DR WPI; 1999-045171/04.
XX
PT New isolated Enterococcus faecalis polynucleotides and polypeptides
PT - used to develop products for the detection of Enterococcus and for
PT use in vaccines for prevention or attenuation of Enterococcus
PT infection.
XX
PS Claim 1; Page 1397-1399; 2084pp; English.
XX
CC A computer readable medium has been developed which has recorded on it
CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
CC AAX12938 to AAX13919 represent these nucleotide sequences which are
CC primary nucleotide sequences, also known as contigs. The computer-based
CC system can identify fragments of the Enterococcus faecalis genome with
CC commercial importance. The products can be used to detect the presence
CC of Enterococcus faecalis in samples. They can also be used for
CC diagnosing Enterococcal infection in an animal and monitoring
CC progression of disease, and for identifying agents which can be used to
CC modulate the growth or pathogenicity of Enterococcus faecalis, or
CC another related organism, in vivo or in vitro. In particular the
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
CC can be used in vaccines to prevent or attenuate an Enterococcal
CC infection.
XX
SQ Sequence 4605 BP; 1371 A; 1019 C; 707 G; 1501 T; 7 other;

Query Match 1.8%; Score 19; DB 20; Length 4605;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 752 accatttttaactgattca 770
||||||||||||||||||
Db 3492 ACCATTTTTAACTGATTCA 3474

RESULT 32
AAH33754
ID AAH33754 standard; cDNA; 291 BP.
XX
AC AAH33754;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:810.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.

```
DR   P-PSDB; AAG74323.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS   Claim 1; Page 2772; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where
CC   the proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene
CC   therapy and vaccine production. N and P may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate P
CC   expression. For example, N and P may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P by expressing
CC   inactive proteins or to supplement the patients own production of P.
CC   Additionally, N may be used to produce the colon cancer-associated Ps,
CC   by inserting the nucleic acids into a host cell and culturing the cell
CC   to express the proteins. N and P can be used in the prevention, diagnosis
CC   and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC   and AAB77789 represent sequences used in the exemplification of the
CC   present invention.
CC   N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC   missing at time of publication, meaning no sequences are present for
CC   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence 291 BP; 86 A; 47 C; 60 G; 96 T; 2 other;


  Query Match              1.7%;  Score 18;  DB 22;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     255 gaaaacacaaccataaat 272
           ||||||||||||||||||
Db     142 gaaaacacaaccataaat 159


RESULT  33
AAX02970
ID   AAX02970 standard; DNA; 1361 BP.
XX
AC   AAX02970;
XX
DT   22-JUN-1999  (first entry)
XX
DE   Human IL-1ra BAC contiguous DNA sequence 15.
XX
KW   Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition;
KW   interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis;
KW   chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease;
KW   growth factors; treatment; IL-1 receptor complex; BAC; ss.
XX
OS   Homo sapiens.
XX
PN   WO9906426-A1.
XX
PD   11-FEB-1999.
XX
PF   03-AUG-1998;   98WO-US16102.
XX
PR   02-JUL-1998;   98US-0091650.
PR   04-AUG-1997;   97US-0054646.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Pan Y;
XX
DR   WPI; 1999-153692/13.
XX
PT   New isolated nucleic acid encoding the new human cytokine Tango-77 -
PT   used to inhibit inflammation and to screen for specific modulators
XX
PS   Example 5; Figure 3; 226pp; English.
XX
CC   AAX02955-X03048 and AAX22301-X22304 are overlapping BAC genomic
CC   sequences containing alternatively spliced forms of human IL-1ra. Such
CC   fragments are used in the method of the invention which describes the
CC   isolation of a novel human TANGO-77 encoding nucleic acid and protein.
CC   Tango-77 is a member of the cytokine superfamily that is expected to
CC   inhibit inflammation by binding to the interleukin-1 receptor (IL-1R). It
CC   may also bind to a new receptor so could regulate other cellular
CC   processes associated with acute or chronic inflammation, e.g. asthma,
CC   chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and
CC   inflammatory bowel disease. It may also induce or suppress interleukins,
CC   cytokines and growth factors. Modulators of this protein are used to
CC   treat or prevent conditions associated with abnormal levels of
CC   inflammation, or activity of IL-1 or its receptor complex.
XX
SQ   Sequence 1361 BP; 462 A; 226 C; 231 G; 442 T; 0 other;


  Query Match              1.7%;  Score 18;  DB 20;  Length 1361;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      49 ttaaatattaactatttc 66
           || ||||||||||||||||
Db     851 ttaaatattaactatttc 868


RESULT  34
AAC75762
ID   AAC75762 standard; cDNA; 1569 BP.
XX
AC   AAC75762;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human ORFX ORF1317 polynucleotide sequence SEQ ID NO:2633.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertensive;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection;
KW   severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US08621.
XX
PR   31-MAR-1999;   99US-0127607.
PR   02-APR-1999;   99US-0127636.
PR   05-APR-1999;   99US-0127728.
PR   30-MAR-2000; 2000US-0540763.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2000-602362/57.
DR   P-PSDB; AAB41553.
```

```
XX
PT   Novel nucleic acids and peptides derived from open reading frame X,
PT   useful for treating e.g. cancers, proliferative disorders,
PT   neurodegenerative disorders and cardiovascular disease -
XX
PS   Claim 5; Page 1878-1879; 5507pp; English.
XX
CC   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC   which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC   sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC   antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC   osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC   immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC   antidiabetic; hypotensive; dermatological; immunosuppressive;
CC   antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC   antithyroid; and antianaemic. The sequences can be used for determining
CC   the presence of or predisposition to, or preventing or treating
CC   pathological conditions associated with an ORFX-associated disorder. The
CC   nucleic acids can be used to express ORFX proteins in gene therapy
CC   vectors. The proteins and nucleic acids may be used to treat cancers,
CC   proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC   graft vs host disease, cardiovascular disease, diabetes mellitus,
CC   hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC   erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC   bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC   allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC   nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC   coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ   Sequence 1569 BP; 356 A; 487 C; 358 G; 367 T; 1 other;


  Query Match             1.7%;  Score 18;  DB 21;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     839 acattcacatgcacacat 856
           ||||||||||||||||||
Db     540 acattcacatgcacacat 557


RESULT  35
AAQ22695/c
ID   AAQ22695 standard; DNA; 1752 BP.
XX
AC   AAQ22695;
XX
DT   24-JUL-1992  (first entry)
XX
DE   Sequence encoding mitochondrial NAD(P)+-dependent malate enzyme.
XX
KW   Carbon metabolism; pyruvate formation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1752
FT                   /*tag=  a
XX
PN   DE4028618-A.
XX
PD   12-MAR-1992.
XX
PF   08-SEP-1990;   90DE-4028618.
XX
PR   08-SEP-1990;   90DE-4028618.
PR   19-JUN-1991;   91DE-4120178.
XX
PA   (BOEH ) BOEHRINGER INGELHEI.
XX
PI   Dworkin MB,  Leober G,  Krystek E,  Maurer-Fogy I;
XX
DR   WPI; 1992-089407/12.
DR   P-PSDB; AAR21845.
XX
PT   Human mitochondrial NAD(P)-dependent malate enzyme - used to
PT   study formation of pyruvate from aminoacid(s) in tumour cells
XX
PS   Claim 2; Page 12-13; 20pp; German.
XX
CC   The inventors claim mitochondrial NAD(P)+-dependent malate enzyme
CC   and DNA encoding it.  AAR21845 has 5' and 3' non-coding regions.  The
CC   enzyme catalyses conversion of malate to pyruvate.  Both the DNA and
CC   the enzyme are useful for studying carbon metabolism in rapidly
CC   dividing cells, esp. pyruvate formation from amino acids.
XX
SQ   Sequence 1752 BP; 562 A; 326 C; 386 G; 478 T; 0 other;


  Query Match             1.7%;  Score 18;  DB 13;  Length 1752;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      77 tggaaaaatataaacatt 94
           |||||||||||||||||
Db    1416 TGGAAAAATATAAACATT 1399


RESULT  36
AAQ23258/c
ID   AAQ23258 standard; DNA; 1923 BP.
XX
AC   AAQ23258;
XX
DT   31-JUL-1992  (first entry)
XX
DE   Mitochondrial NAD(P)+-dependent malate enzyme.
XX
KW   C-metabolism; tumour; pyruvate; T-lymphocyte; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1844
FT                   /*tag=  a
FT                   /product= malate_enzyme
FT   sig_peptide     90..149
FT                   /*tag=  b
FT   mat_peptide     150..1844
FT                   /*tag=  c
FT   polyA_signal    1905..1910
FT                   /*tag=  d
FT                   /note= "homologous to poly(A) signal AATAAA"
XX
PN   WO9204448-A.
XX
PD   19-MAR-1992.
XX
PF   23-AUG-1991;   91WO-EP01602.
XX
PR   19-JUN-1991;   91DE-4120178.
PR   08-SEP-1990;   90DE-4028618.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM.
XX
PI   Dworkin MB,  Loeber G,  Krystek E,  Maurerfog I,  Fruhbeis B;
XX
DR   WPI; 1992-114355/14.
DR   P-PSDB; AAR22356.
XX
PT   New human mitochondrial malate enzyme and DNA encoding it - for
PT   studying carbon metabolism in cells, also specific antibodies for
PT   purificn. and assay
XX
PS   Claim 1; Page 46 + Fig 3; 60pp; German.
XX
```

```
CC   The sequence may be used to study C-metabolism in rapidly dividing
CC   (tumour) cells, esp. pyruvate formation from amino acids.
CC   The enzyme was first isolated from the supernatant of mitochondrial
CC   preparations from the transformed human T-lymphocyte cell line
CC   1301.  Tryptic fragments were partially sequenced and used as a
CC   basis for the design of oligonucleotides.  These were used in PCR
CC   for amplification of malate enzyme encoding DNA in a cDNA bank
CC   prepd. from fibrosarcoma HS913.  Amplified fragments were subcloned
CC   in pUC18, sequenced and used to probe the fibrosarcoma bank.
CC   A 1923bp insert was isolated and cloned in Bluescript KS+.
CC   The poly(A+) tail is not included in this sequence.
XX
SQ   Sequence 1923 BP; 598 A; 373 C; 436 G; 516 T; 0 other;


  Query Match             1.7%;  Score 18;  DB 13;  Length 1923;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      77 tggaaaaatataaacatt 94
           ||||||||||||||||||
Db    1505 TGGAAAAATATAAACATT 1488


RESULT  37
AAF18038/c
ID   AAF18038 standard; DNA; 2033 BP.
XX
AC   AAF18038;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Lung cancer associated polynucleotide sequence SEQ ID 57.
XX
KW   Human; lung cancer associated protein; neuroprotective; cytostatic;
KW   cardioactive; immunomodulatory; muscular active; vulnerary;
KW   gastrointestinal; nephrotropic; antiinfective; gynecological;
KW   antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW   proliferative disorder; wound healing; infectious disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055180-A2.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05918.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Ruben SM;
XX
DR   WPI; 2000-587514/55.
DR   P-PSDB; AAB58162.
XX
PT   Lung cancer associated gene sequences, referred to as lung cancer
PT   antigens, useful for treatment, prevention, and diagnosis of disorders
PT   such as lung cancer -
XX
PS   Claim 1; Page 536-537; 1425pp; English.
XX
CC   Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC   associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC   associated proteins and polynucleotide sequences, their agonists, and
CC   antagonists may have neuroprotective; cytostatic; cardioactive;
CC   immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC   general; nephrotropic; antiinfective; gynecological; or antibacterial
CC   activity. The invention also includes antibodies specific for the
CC   protein or polynucleotide sequences. The lung cancer associated
CC   polynucleotide sequences may be used for detection of lung cancer,
CC   chromosome identification, as chromosome markers, and for numerous other
CC   diagnostic or research purposes. The proteins may be used to treat
CC   disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders. The proteins may also be used in the treatment of wounds and
CC   infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC   peptide AAB58549 are used in the course of the invention for the
CC   identification and characterisation of the polynucleotide and protein
CC   sequences.
XX
SQ   Sequence 2033 BP; 399 A; 623 C; 628 G; 370 T; 13 other;


  Query Match             1.7%;  Score 18;  DB 21;  Length 2033;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     720 ctgactctggagcctctt 737
           ||||||||||||||||||
Db    1902 CTGACTCTGGAGCCTCTT 1885


RESULT  38
AAQ13822/c
ID   AAQ13822 standard; cDNA; 3060 BP.
XX
AC   AAQ13822;
XX
DT   10-DEC-1991  (first entry)
XX
DE   Human GAP b3 gene.
XX
KW   Galactoprotein b3; carcinoma; cancer; tumour; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3060
FT                   /*tag=  a
XX
PN   WO9113983-A.
XX
PD   19-SEP-1991.
XX
PF   08-APR-1991;   91WO-US01606.
XX
PR   12-MAR-1990;   90US-0491910.
XX
PA   (BIOM-) BIOMEMBRANE INST.
XX
PI   Tsuji T,  Yamamoto F,  Hakomori S;
XX
DR   WPI; 1991-295637/40.
DR   P-PSDB; AAR14118.
XX
PT   DNA sequences encoding galactoprotein b3 - produced using DNA
PT   constructs also antibodies to Gap b3 used to detect tumours that
PT   result in elevated expression of protein.
XX
PS   Claim 1; Fig 6; 46pp; English.
XX
CC   The sequence was obtd. from 3 overlapping clones isolated from
CC   a human I24 cell line cDNA library. The DNA can be used to express
CC   the Gap b3 protein which is a transformation-dependent cell surface
CC   glycoprotein.  The protein may be used to produce antibodies and
CC   these, or the DNA sequences, can be used to detect and quantify
CC   levels of Gap b3 protein or mRNA in biological samples. A high
CC   level of the protein is indicative of certain cancers.
CC   See also AAQ13821-Q13824.
XX
SQ   Sequence 3060 BP; 643 A; 913 C; 910 G; 594 T; 0 other;
```

```
  Query Match             1.7%;  Score 18;  DB 12;  Length 3060;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     507 cttctgctgctgctctga 524
           ||||||||||||||||||
Db    1818 CTTCTGCTGCTGCTCTGA 1801


RESULT  39
AAV23920/c
ID   AAV23920 standard; DNA; 4636 BP.
XX
AC   AAV23920;
XX
DT   31-JUL-1998  (first entry)
XX
DE   Human alpha3 integrin coding sequence.
XX
KW   Anti-integrin alpha3 antibody; human; anti-tumour agent;
KW   chemotherapeutic drug; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73..3228
FT                   /*tag= a
XX
PN   WO9809651-A1.
XX
PD   12-MAR-1998.
XX
PF   03-SEP-1997;   97WO-JP03085.
XX
PR   03-SEP-1996;   96JP-0250887.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Hayakawa T,  Kawata H,  Sekimori Y,  Shimizu K,  Tominaga E;
XX
DR   WPI; 1998-193327/17.
DR   P-PSDB; AAW54032.
XX
PT   Anti-integrin alpha3 antibody and chemotherapeutic drug - useful in
PT   anti-tumour agents and diagnostic reagent compositions
XX
PS   Disclosure; Page 68-76; 96pp; Japanese.
XX
CC   This sequence encodes the human alpha3 integrin protein. The alpha3
CC   integrin sequence is targeted by the anti-integrin alpha3 antibody of the
CC   invention. The anti-integrin alpha 3 antibody or its antigen binding
CC   fragment are for use as anti-tumour agents, and diagnostic reagent
CC   compositions. They can also be used in a chemotherapeutic drug.
XX
SQ   Sequence 4636 BP; 961 A; 1452 C; 1336 G; 887 T; 0 other;


  Query Match             1.7%;  Score 18;  DB 19;  Length 4636;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     507 cttctgctgctgctctga 524
           ||||||||||||||||||
Db    1986 CTTCTGCTGCTGCTCTGA 1969


RESULT  40
AAA68247/c
ID   AAA68247 standard; DNA; 41708 BP.
XX
AC   AAA68247;
XX
DT   27-OCT-2000  (first entry)
XX
DE   Bacteriophage 77 complete genome sequence.
XX
KW   Bacteriophage; antimicrobial; genome; identification; antibacterial;
KW   bacterial growth inhibition; bacterial infection; ds.
XX
OS   Bacteriophage 77.
XX
PN   WO200032825-A2.
XX
PD   08-JUN-2000.
XX
PF   03-DEC-1999;   99WO-IB02040.
XX
PR   03-DEC-1998;   98US-0110992.
PR   03-JUN-1999;   99US-0326144.
PR   28-SEP-1999;   99US-0407804.
PR   30-SEP-1999;   99US-0157218.
PR   01-DEC-1999;   99US-0168777.
PR   02-DEC-1999;   99US-0454252.
XX
PA   (PHAG-) PHAGETECH INC.
XX
PI   Pelletier J,  Gros P,  Dubow M;
XX
DR   WPI; 2000-412361/35.
XX
PT   Identifying a bacteriophage coding region for treating bacterial
PT   infections comprises identifying a nucleic acid encoding a product that
PT   inhibits bacteria when a bacteriophage infects a bacterium
XX
PS   Example 3; Page 141-151; 456pp; English.
XX
CC   The present invention describes a method for identifying a bacteriophage
CC   coding region encoding a product active on an essential bacterial
CC   target. The method comprises identifying a nucleic acid sequence encoding
CC   a gene product that provides a bacteria-inhibiting function when an
CC   uncharacterised bacteriophage infects a pathogenic bacterium. The
CC   compound active on a target of a bacteriophage inhibitor protein in a
CC   bacteria is used to treat or prevent a bacterial infection in an animal.
CC   AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage
CC   nucleotide and protein sequences which are used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 other;


  Query Match             1.7%;  Score 18;  DB 21;  Length 41708;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     957 cttcatgacctgtaataa 974
           ||||||||||||||||||
Db   30283 CTTCATGACCTGTAATAA 30266


RESULT  41
AAC86106/c
ID   AAC86106 standard; cDNA; 41708 BP.
XX
AC   AAC86106;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Complete genome of bacteriophage 77.
XX
KW   DnaI; S. aureus; inhibitor; bacteriophage 77; ORF 104; phage 77ORF104;
KW   screening assay; ss.
XX
OS   Bacteriophage 77.
XX
PN   WO200146383-A2.
XX
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```
PD   28-JUN-2001.
XX
PF   21-DEC-2000; 2000WO-US35180.
XX
PR   22-DEC-1999;   99US-0470512.
PR   12-OCT-2000; 2000US-0689952.
XX
PA   (PHAG-) PHAGETECH INC.
PA   (WILL/) WILLIAMS K M.
XX
PI   Pelletier J,  Gros P,  Dubow M;
XX
DR   WPI; 2001-418052/44.
XX
PT   Novel DnaI polypeptides useful for treating and diagnosing microbial,
PT   preferably bacterial, diseases such as those caused by Staphylococcus
PT   aureus -
XX
PS   Disclosure; Fig 2; 107pp; English.
XX
CC   This sequence represents the genome of Bacteriophage 77.  The
CC   growth inhibitory gene product of ORF 104 interacts with DnaI derived
CC   from S. aureus, to form the basis of a screening assay.  DnaI
CC   polypeptides and polynucleotides are useful for treating microbial,
CC   preferably bacterial, especially Staphylococcal, infections. DnaI
CC   polypeptides and polynucleotides are useful for biological, diagnostic,
CC   prophylactic, clinical and therapeutic use, and as components in
CC   databases useful for search analyses as well as in sequence analysis
CC   algorithms.
XX
SQ   Sequence 41708 BP; 15607 A; 5898 C; 8088 G; 12115 T; 0 other;


  Query Match             1.7%;  Score 18;  DB 22;  Length 41708;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     957 cttcatgacctgtaataa 974
           ||||||||||||||||||
Db   30283 CTTCATGACCTGTAATAA 30266


RESULT  42
AAC31204
ID   AAC31204 standard; cDNA; 212 BP.
XX
AC   AAC31204;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 35279.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 35279; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 212 BP; 64 A; 41 C; 40 G; 66 T; 1 other;


  Query Match             1.6%;  Score 17;  DB 21;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     967 tgtaataatctcataat 983
           |||||||||||||||||
Db      43 tgtaataatctcataat 59


RESULT  43
AAC10699
ID   AAC10699 standard; cDNA; 314 BP.
XX
AC   AAC10699;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 14774.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 14774; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
```

```
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 314 BP; 102 A; 68 C; 44 G; 100 T; 0 other;


  Query Match             1.6%;  Score 17;  DB 21;  Length 314;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      46 attttaaatattaacta 62
           ||||||||||||||||
Db     216 attttaaatattaacta 232


RESULT  44
AAH71986
ID   AAH71986 standard; cDNA; 329 BP.
XX
AC   AAH71986;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Human cervical cancer marker nucleic acid 3260.
XX
KW   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142467-A2.
XX
PD   14-JUN-2001.
XX
PF   08-DEC-2000; 2000WO-US33312.
XX
PR   08-DEC-1999;   99US-0169681.
PR   21-DEC-1999;   99US-0171350.
PR   14-MAR-2000; 2000US-0189315.
PR   12-MAY-2000; 2000US-0203791.
PR   09-JUN-2000; 2000US-0210600.
PR   21-JUL-2000; 2000US-0220114.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Deeds J,  Berger A,  Zhao X;
XX
DR   WPI; 2001-375006/39.
XX
PT   New isolated nucleic acid for diagnosing and treating cervical cancer
PT   and for assessing and detecting compounds for treating the cancer -
XX
PS   Claim 1; Page 639; 1051pp; English.
XX
CC   The invention relates to novel genes (AAH68727-AAH73383) associated with
CC   cervical cancer with cytostatic activity. The nucleic acids and encoded
CC   polypeptides are useful: to assess if a patient is afflicted with
CC   cervical cancer or has a pre-malignant condition; to monitor the
CC   progression of cervical cancer or a premalignant condition in a patient;
CC   and to select and/or assess the efficacy of a compound or therapy for
CC   inhibiting cervical cancer in a patient. The nucleic acids may also be
CC   useful for gene therapy.
XX
SQ   Sequence 329 BP; 117 A; 55 C; 70 G; 87 T; 0 other;


  Query Match             1.6%;  Score 17;  DB 22;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     384 tgaaaagcattttacaa 400
           ||||||||||||||||
Db      55 tgaaaagcattttacaa 71


RESULT  45
AAC54948/c
ID   AAC54948 standard; DNA; 396 BP.
XX
AC   AAC54948;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 79643.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
PR   14-MAY-1999;   99US-0134221.
PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
PR   20-MAY-1999;   99US-0135124.
PR   21-MAY-1999;   99US-0135353.
PR   24-MAY-1999;   99US-0135629.
PR   25-MAY-1999;   99US-0136021.
PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
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Query Match 1.6%; Score 17; DB 21; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
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Qy 886 aaaaggaataatctctt 902
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Db 321 AAAAGGAATAATCTCTT 305

Search completed: April 30, 2002, 10:55:50
Job time: 11019 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 30, 2002, 10:55:50 ; Search time 728.83 Seconds
(without alignments)
1177.480 Million cell updates/sec

Title: US-09-248-178-64
Perfect score: 1001
Sequence: 1 gaatgtgcaacgatcaagtc.....ctaccaaaaaaaaaaaaaaa 1001

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 10

Total number of hits satisfying chosen parameters: 416337

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1001	100.0	1001	20	AAX84210	DNA encoding human
	2	1001	100.0	1001	21	AAC79439	cDNA sequence of h
	3	373	37.3	3101	21	AAC79472	cDNA sequence of h
c	4	32	3.2	305	21	AAC27257	Human secreted pro
	5	30	3.0	41100	22	AAS10873	Human genomic DNA
	6	29	2.9	1308	21	AAC59199	Human secreted pro
c	7	27	2.7	319	14	AAQ59633	Human brain Expres
	8	27	2.7	1177	22	AAF92122	Human PRO1928 cDNA
	9	27	2.7	1182	22	AAD05647	Human secreted pro
	10	27	2.7	1917	22	AAD05599	Human secreted pro
	11	27	2.7	2781	22	AAH73960	Human helix-destab
	12	27	2.7	10409	19	AAV42558	Mouse dectin-2 gen
	13	27	2.7	29604	18	AAX83005	Partial mouse WRN
c	14	27	2.7	44576	21	AAZ61522	Cosmid CVO14 conta
	15	25	2.5	535	22	AAI16817	Probe #6750 for ge
	16	25	2.5	535	22	AAI40430	Probe #9116 used t
	17	25	2.5	554	22	AAI16533	Probe #6466 for ge
	18	25	2.5	554	22	AAI39509	Probe #8195 used t
	19	25	2.5	27150	22	AAD02701	Human glycosyl sul
	20	25	2.5	144460	21	AAZ93815	Olfactory receptor
	21	25	2.5	319608	21	AAH51601	Human chromosome 1
	22	25	2.5	319608	22	AAS09301	Human schizophreni
	23	24	2.4	305	21	AAC28302	Human secreted pro
	24	24	2.4	48000	22	AAF27996	Human calcium sens
c	25	24	2.4	160271	22	AAS04858	Human chromosome 1
c	26	24	2.4	160271	22	AAS04864	Human chromosome 1
c	27	24	2.4	160271	22	AAS06667	Human chromosome 1
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c	29	24	2.4	160271	22	AAH23764	Human chromosome 1
c	30	24	2.4	160271	22	AAF85116	Nucleotide sequenc
	31	23	2.3	553	22	AAF93676	cDNA isolated from
c	32	23	2.3	1001	21	AAC57891	Arachidonic acid m
	33	23	2.3	5353	22	AAD04475	Human 27875 ADAM-T
	34	23	2.3	5353	22	AAD04494	Human 27875 ADAM-T
c	35	23	2.3	80331	22	AAC89559	Human histone deac
	36	22	2.2	247	21	AAC15149	Human secreted pro
	37	22	2.2	329	21	AAC26972	Human secreted pro
	38	22	2.2	329	21	AAZ42729	Human 5' EST isola
	39	22	2.2	731	21	AAC36471	Arabidopsis thalia
	40	22	2.2	1005	20	AAZ22862	Wheat indole-3-gly
	41	22	2.2	1148	21	AAC32953	Arabidopsis thalia
c	42	22	2.2	1796	22	AAH17506	Human cDNA sequenc
	43	22	2.2	8654	15	AAQ55138	Staphylococcus epi
	44	22	2.2	11617	22	AAI62937	Human genomic DNA
	45	22	2.2	11722	19	AAV34455	Human MHC class I

ALIGNMENTS

RESULT 1
AAX84210
ID AAX84210 standard; cDNA; 1001 BP.
XX
AC AAX84210;
XX
DT 08-SEP-1999 (first entry)
XX
DE DNA encoding human breast tumour protein immunogenic fragment.
XX
KW Breast tumour protein; immunogenic fragment; vaccine; detection;
KW breast cancer development; therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9933869-A2.
XX
PD 08-JUL-1999.
XX
PF 22-DEC-1998; 98WO-US27416.
XX
PR 17-JUL-1998; 98US-0118627.
PR 24-DEC-1997; 97US-0998253.
PR 24-DEC-1997; 97US-0998255.
PR 17-JUL-1998; 98US-0118554.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J;
XX
DR WPI; 1999-405486/34.
XX
PT New breast tumour protein genes used, in vaccines for immunotherapy,
PT or for diagnosis of breast cancer

```
XX
PS   Claim 3; Page 61; 70pp; English.
XX
CC   This sequence encodes a human breast tumour protein immunogenic fragment
CC   of the invention. The polypeptides or nucleic acids encoding them are
CC   useful in vaccines and pharmaceutical compositions for manufacture of
CC   medicaments for inhibiting the development of breast cancer in a patient.
CC   They can also be used to treat breast cancer. Antibodies against these
CC   polypeptides can be used to detect and monitor progression of breast
CC   cancer in patients. Primers and probes derived from the polynucleotides
CC   encoding the breast proteins are useful for detection of breast cancer.
CC   Peripheral blood cells from a patient incubated in the presence of at
CC   least one polypeptide, such that T cells proliferate, are useful in
CC   manufacture of a medicament for treating breast cancer in a patient.
CC   Antigen presenting cells incubated in the presence of at least one
CC   polypeptide are also useful for treating breast cancer.
XX
SQ   Sequence 1001 BP; 278 A; 159 C; 160 G; 404 T; 0 other;

  Query Match             100.0%;  Score 1001;  DB 20;  Length 1001;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy     181 ggtttgtattcatttaccaccctcttttcattcccttttctcacccacacactgtgccggg 240
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Qy     241 cctcaggcatatactattctactgtctgtctctgtaaggattatcattttagcttccaca 300
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Qy     361 gacctccgcttccatccatgttatttatattacccaatagtgttcataaatatatataca 420
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Qy     421 cacatatataccacattgcatttgtccaattattcattgacggaaactggttaatgttat 480
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Qy     481 atcgttgctattgtggatagtgctgcaataaacacgcaagtggggatataatttgaagag 540
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Qy     781 agatcaagtgtattccctaaatattttatttttgtagctattgtagatgaaattgccttc 840
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RESULT   2
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ID   AAC79439 standard; cDNA; 1001 BP.
XX
AC   AAC79439;
XX
DT   07-FEB-2001  (first entry)
XX
DE   cDNA sequence of human breast tumour clone 1012H8.
XX
KW   Human; breast tumour antigen; cytostatic; immunotherapy;
KW   breast cancer; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061756-A2.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US09688.
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PR   09-APR-1999;   99US-0288950.
PR   02-JUL-1999;   99US-0346327.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Reed SG,  Xu J,  Dillon DC;
XX
DR   WPI; 2000-636568/61.
XX
PT   A novel isolated polypeptide comprising an immunogenic portion of a
PT   breast cancer protein useful in the detection and treatment of breast
PT   cancer
XX
PS   Claim 4; Page 77-78; 95pp; English.
XX
CC   The present sequence was isolated from a breast tumour cDNA library. It
CC   is provided in a specification relating to compounds for immunotherapy
CC   and diagnosis of breast cancer. Breast tumour antigens and the
CC   polynucleotides that encode them may be used in the production of a
CC   pharmaceutical composition to be used in the treatment of breast cancer.
CC   Proliferated T cells and incubated antigen presenting cells are also
CC   required. The polypeptides and polynucleotides may also be used to
CC   produce a vaccine.
XX
SQ   Sequence 1001 BP; 278 A; 159 C; 160 G; 404 T; 0 other;


  Query Match             100.0%;  Score 1001;  DB 21;  Length 1001;
  Best Local Similarity   100.0%;  Pred. No. 0;
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